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Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile	20	25	30
Thr Gly Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser	35	40	45
Leu Glu Asn Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val	50	55	60
Pro Phe Val Leu Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly	65	70	75
Thr Phe Gly Cys Phe Ala Thr Cys Arg Ala Ser Ala Trp Met Leu	80	85	90
Lys Leu Tyr Ala Met Phe Leu Thr Leu Val Phe Leu Val Glu Leu	95	100	105
Val Ala Ala Ile Val Gly Phe Val Phe Arg His Glu Ile Lys Asn	110	115	115
Ser Phe Lys Asn Asn Tyr Glu Lys Ala Leu Lys Gln Tyr Asn Ser	125	130	135
Thr Gly Asp Tyr Arg Ser His Ala Val Asp Lys Ile Gln Asn Thr	140	145	150
Leu His Cys Cys Gly Val Thr Asp Tyr Arg Asp Trp Thr Asp Thr	155	160	165
Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser Cys Cys Lys Leu	170	175	180
Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val Asn Asn Glu	185	190	195
Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu Met Gly	200	205	210
Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu Ile	215	220	225
Gly Ile Phe Leu Ala Tyr Cys Xaa Ser Arg Ala Ile Thr Asn Asn	230	235	240
Gln Tyr Glu Ile Val	245		

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 330 ctgcgcaag cttgtgtcca cagggcaaaag gagaatattt taatgctccg 1100
 340 ctgatggcag agtaaatgat aagatttgat gtttttgctt gctgtcatct 1150
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 <222> 22-26, 50-54, 113-117
 <223> Casein Kinase II Phosphorylation Site.

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 35 40 45
 Lys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln
 50 55 60
 Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser
 65 70 75
 Glu Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro
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Phe	Gly	Leu	Val	Gln	Ser	Lys	Leu	Phe	Pro	Phe	Tyr	Phe	His	Ile
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Ser	Met	Gly	Cys	Ala	Phe	Ile	Asn	Leu	Cys	Ile	Leu	Ala	Ser	Gln
				65					70					75
His	Ala	Trp	Ala	Gln	Leu	Thr	Phe	Trp	Glu	Ala	Ser	Gln	Leu	Tyr
				80					85					90
Leu	Leu	Phe	Leu	Ser	Leu	Thr	Leu	Ala	Thr	Val	Asn	Ala	Arg	Trp
				95					100					105
Leu	Glu	Pro	Arg	Thr	Thr	Ala	Ala	Met	Trp	Ala	Leu	Gln	Thr	Val
				110					115					120
Glu	Lys	Glu	Arg	Gly	Leu	Gly	Gly	Glu	Val	Pro	Gly	Ser	His	Gln
				125					130					135
Gly	Pro	Asp	Pro	Tyr	Arg	Gln	Leu	Arg	Glu	Lys	Asp	Pro	Lys	Tyr
				140					145					150
Ser	Ala	Leu	Arg	Gln	Asn	Phe	Phe	Arg	Tyr	His	Gly	Leu	Ser	Ser
				155					160					165
Leu	Cys	Asn	Leu	Gly	Cys	Val	Leu	Ser	Asn	Gly	Leu	Cys	Leu	Ala
				170					175					180
Gly	Leu	Ala	Leu	Glu	Ile	Arg	Ser	Leu						
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 tacatttitta tcactggatg tgactcgagg ttfggaaact tggcagccag 250
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 Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
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 Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
 65 70 75
 Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
 80 85 90
 Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
 95 100 105
 Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
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 Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
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 Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
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 Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
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 Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys
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 185 190 195

210 Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Ile Lys
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 9980
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 cctcctggcc gccccgaggg gggcttggag ggtcggaagg caagtcctc 2650
 tagtccagg gccctccag tggaatgggt cttttcggtg gagataaaag 2700
 ttgatttgc ctaacggcaa 2720

210 12
 211 639
 212 PRT
 213 Homo sapiens

220
 221 TRANSMEM
 222 21-40 and 84-105
 223 Transmembrane Domain (type II)

400 12
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser
 1 5 10 15
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
 20 25 30
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

Asp His Trp Lys	Ala Leu Ala Phe Arg	Leu Glu Glu Glu Glu Lys	110	111	112
Met Arg Pro Glu	Ile Ala Gly Leu Lys	Pro Ala Asn Pro Pro Val	125	127	128
Leu Pro Ala Pro	Gln Lys Ala Asp Thr	Asp Pro Glu Asn Leu Pro	140	141	150
Glu Ile Ser Ser	Gln Lys Thr Gln Arg	His Ile Gln Arg Gly Pro	151	159	168
Pro His Leu Gln	Ile Arg Pro Pro Ser	Gln Asp Leu Lys Asp Gly	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg Gln	Gln Ala Pro Val Asp Pro	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg Thr	Val Ile Ser Trp Arg Gly	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly Thr	Gln Leu Pro Ser Arg Arg	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro Leu	Pro Pro Ala Arg Thr Gln	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr Arg	Gln Lys Gly Val Ile Asp	245	250	255
Val Phe Leu His	Ala Trp Lys Gly Tyr	Arg Lys Phe Ala Trp Gly	260	265	270
His Asp Glu Leu	Lys Pro Val Ser Arg	Ser Phe Ser Glu Trp Phe	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp Ala	Leu Asp Thr Met Trp Ile	290	295	300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val Ser	305	310	315
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe Glu	320	325	330
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His Leu	335	340	345
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly Asn	350	355	360
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr Ser	365	370	375
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp Thr	380	385	390
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu Phe			

Arg Glu Leu Ser	Arg Leu Thr Gly Asp	Lys Lys Phe Gln Glu Ala
410	415	420
Val Glu Lys Val	Thr Gln His Ile His	Gly Leu Ser Gly Lys Lys
425	430	435
Asp Gly Leu Val	Pro Met Phe Ile Asn	Thr His Ser Gly Leu Phe
440	445	450
Thr His Leu Gly	Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser Tyr
455	460	465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln Glu
470	475	480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val Arg
485	490	495
Thr His Leu Leu	Arg His Ser Glu Pro	Ser Lys Leu Thr Phe Val
500	505	510
Gly Glu Leu Ala	His Gly Arg Phe Ser	Ala Lys Met Asp His Leu
515	520	525
Val Cys Phe Leu	Pro Gly Thr Leu Ala	Leu Gly Val Tyr His Gly
530	535	540
Leu Pro Ala Ser	His Met Glu Leu Ala	Gln Glu Leu Met Glu Thr
545	550	555
Cys Tyr Gln Met	Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro Glu
560	565	570
Ile Val His Phe	Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp Val
575	580	585
Glu Val Lys Pro	Ala Asp Arg His Asn	Leu Leu Arg Pro Glu Thr
590	595	600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg Lys
605	610	615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg Phe
620	625	630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val Gln
635	640	645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe Phe
650	655	660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp Asp
665	670	675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr	Val Phe Asn Thr Gln Ala
680	685	690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cggagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgaagt gtttggcctc ggtc 44

<210> 16
<211> 1504
<212> DNA
<213> Homo sapiens

<400> 16
ggcaccggt aggcacggga ggcagggcgg gccggggtgc gagcgctgc 50
cccatggccc gcgcctctc cgcacgatgt tccctcgcg gaggaagcg 100
ggcagctac cctgggagga ggcaggtcc gggttgctct ccggcggt 150
cctcgggaag tgttcgtct tccactgtt cgtggctac ctctcgctgg 200
gtttctctc cctactctgg ctgcactca cctctctgg ggaactggc 250

tgggtgttca ggggaaanaa maagaaac tgggacata tgggtgacta 390
 cccccagag cggccccctg agcactggga agaagaagga ttttggggag 395
 ccccccctt ggcagtgttg gtgactttcc ggcgaacgatt agaggagctc 400
 ctggttcttg tgcaccacat ggcgggcttc ctgagcagga agaagatcag 450
 acacacata tacttgctca accagggtga caacttcagg ttaaacggg 500
 caagctcat caacgtgggc ttctggaga gcagcaacag caaggactac 550
 attgcacag aagacgttga cctgtccctt ctcaacgagg agctggacta 600
 tgggtttctt gaggttgggc ccttcaagt ggcctcccg gagctccac 650
 ctctctacca ctacaagac tatgtcggg gcaccttgt gctctcaag 700
 cagcactacc ggtgtgtcaa tgggatgtcc aacggcttct ggggttggg 750
 ccggaggagc gacagttct accggggcat taaggagct gggctccagc 800
 tttccggcc ctgggaata caaactgggt caaagacatt tgcacacctg 850
 catgaaccag cctgggggaa gagggaacag aagcgcctcg cagctcaaaa 900
 acaggagcag ttaagggtg acagggagg aggcctgaac actgtgaagt 950
 accatgtggc ttcgggact ggcctgtctg tggggggg ccctgcact 1000
 gtctcaaca ccatgttggc ctgtgacaag accgcaacac cctggtgcac 1050
 attcagctga gctggatga cagtgaaggc gctgtactt acaggccata 1100
 ttgtcaggc ccaggacaag gctcaggtc gtggggccag ctctgacagg 1150
 atgtggagtg gccaggacca agacagcaag ctacgcaatt gcagcaaccc 1200
 ggcggccaag gcaggcttgg gctgggacag gacacgtggg gtgcctggga 1250
 cgtgtcttgc catgcacagt gatcagag aggttgggt gtgtcctgtc 1300
 cgggaccccc cctgccttcc tgcacacct actctgaact ccttcagtg 1350
 accaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400
 cctactctga cctccttcac gtgcacaggc ctgtgggtag tgggagggc 1450
 tgaacagac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<10> 1'
 <11> 329
 <12> FRT
 <13> Homo sapiens

<22>

<118 sig_peptide
 <222 1-40
 <223 Signal peptide.

 <220
 <221 misc_feature
 <222 19-25,65-71,247-253,285-291,303-310
 <223 N-myristoylation site.

 <220
 <221 misc_feature
 <222 27-31
 <223 cAMP- and cGMP-dependent protein kinase phosphorylation site.

 <220
 <221 TRANSMEM
 <222 29-49
 <223 Transmembrane domain (type II).

 <220
 <221 misc_feature
 <222 154-158
 <223 N-glycosylation site.

 <220
 <221 misc_feature
 <222 226-233
 <223 Tyrosine kinase phosphorylation site.

 <400 17
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1 5 10 15
 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
 20 25 30
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
 50 55 60
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
 65 70 75
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
 80 85 90
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
 95 100 105
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
 110 115 120
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
 125 130 135
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

140	145	150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile	Ala Met His Asp Val Asp	
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu Ala	
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu	Leu His Pro Leu Tyr His	
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln His	
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp Gly	
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly Leu	
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr Phe	
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys Arg	
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu Gly	
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val	Ala Ser Arg Thr Ala Leu	
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val	Leu Asn Ile Met Leu Asp	
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys	Thr Phe Ser	
320	325	

<210> 18

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 18

cgagaagcctt cgaggagtaa tgg 23

<410> 19

<411> 24

<412> DNA

<413> Artificial

<420>

<421> Artificial Sequence

<22> 1-24
<23> Synthetic construct

<200> 19
gcaatgcggg aagccacatg ctac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<231> Artificial Sequence
<232> 1-46
<233> Synthetic construct.

<400> 10
cttctctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 11
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccact cccccaagcc cctttacctt tgcctcgtgt 50
aagcctgctg ctgcctgctg tgcctgttaa aggcctcatg ttggagtggg 100
gattggtggg tgcacagaaa gtctctttct ccactgagcg cccnctcagg 150
gattgacct tctttccccc ttcttttttg tgtctctctg ctcatcgccc 200
tgcctatacc tgnagccaaag cccagccccg tgggggaaggg gagaaagtgg 250
ggatctgcta agaaagctgg gagataggga acagaagagg gtatggggtg 300
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
atttatccaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctctgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450
taaacattta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 21
<211> 77
<212> PRT
<213> Homo sapiens

<210>
<211> sig_peptide
<212> 1-15
<213> Signal peptide.

<210>
<211> misc_feature
<212> 3-18

<210> Growth factor and cytokines receptors family.

<211> 127

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
5 10 15

Pro Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Ile Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 13

<211> 1883

<212> DNA

<213> Homo sapiens

<400> 23

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ccataagggt cccgtccccc ctgggccccg gcgcgcctcc tgcccccccg 150

ggtccggggg aggcctgcta ggcagtgag ccgcgcctcg cccgcagggc 200

cccgccccc agcatggagc cacccggaag cccggggggc cgcgcgcagc 250

cgcgcctgtt gctgcgcctc ccgcctgttg cgcctgcgcg gctgcctggg 300

ggggggggcg cggggggcgc cgggggcctg cccgcggggt gcaagcacga 350

ggggggggcc cagggggctg gcaggggggc gggggccgcc gagggcaagg 400

tggtgtgcag cagcctggaa ctgcgcagg tctgccccc agataactcg 450

cccaaccgca cggtcacct gattctgagt aacaataaga tatccagctc 500

gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttgacctcc 550

gaaacaatct tattagtagt atagatccag ctgccttctg gggactgtca 600

tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650

agacataatt cagggactca ccaatcttgt ccggctaaac ctttcgggga 700

atttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750

aggtctttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800

gagpatgcac cgtatgttaa adagagaaga catcaggtta ccgcatacca 850

ttttaa aaattttat ttttttttaa gttttttat ttgttttttt 2350
 tttttttt ttaagaaat agatgtttt tatggggccc taaaagtatc 2400
 tttttt ggaactggc ctccacagcc tagtggagaa gtcaacctg 2450
 tttttgtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500
 ttttat gtcatatata tttttttaaa aaaagtattt cattgaagca 2550
 tttttatga aagcattttt actgattttt aaaattgggtg ctttagatat 2600
 tttttttac actgtattga agcaaataga ggaggacaaa ctccagcacc 2650
 tttttgaac cacattttt tcaattagct ttctgtgggc atgtgtaatt 2700
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 tcttttat cacaaaat attccagtc ttttaatggc tgcataataa 2800
 ctcttcaac aggtgttagg tgtttctggt tagtgtgagc actcaataaa 2850
 tattgatga atgaacgaaa aaaaaaaaaa aaa 2883

<210> 24
 <211> 616
 <212> PPT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-33
 <223> Signal peptide.

<220>
 <221> TRANSMEM
 <222> 13-40
 <223> Transmembrane domain (type II).

<400> 24
 Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu
 1 5 10 15
 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
 35 40 45
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
 50 55 60
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
 65 70 75
 Ser Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
 80 85 90

100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
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Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
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Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
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Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg						
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Trp Arg Asp Asp Asp Tyr Ser Arg Cys Gln Tyr Ala Asn Asp Val		
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Phe Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr		
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Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu		
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Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys		
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Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu		
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Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala		
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Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg		
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Leu Ala Gly Gly Ala His Val Tyr Ser Thr Tyr Ser Pro Asn Ile		
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Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met		
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Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly		
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Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys		
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Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu		
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Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr		
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0211> 24

0212> RNA

0213> Artificial

0220>

0221> Artificial Sequence

0222> 1-24

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<400> 26

<400> 24

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<400> Artificial Sequence

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<400> 26

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<400> 27

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<400> 28

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 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
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 tccatgcatc cctctgctaa gaccgtgccc atgcacgtga cggtaaccgg 150
 caccaccatc acaacaccca cgaactcacc ttggggcttg gggccccca 200
 tgaatgtggg gtcacatcgg gacctgacac agcccttggg tctccttggc 250
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Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Irc	Phe	Phe	Ser	Phe	Leu	
				240				235						245	
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	
				245				250						255	
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	
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Irc	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	
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Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	
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Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala	
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His	Leu	Val	Phe	Val	Lys	Val									
				320											

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 <212> DNA
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Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser
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Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu
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Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser
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			335											

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 4213> Artificial

4220>
 4221> Artificial Sequence
 4222> 1-25
 4223> Synthetic construct

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4410> 35
 4411> 50
 4412> DNA
 4413> Artificial

4420>
 4421> Artificial Sequence
 4422> 1-50
 4423> Synthetic construct.

4400> 35
 4400>atggatacta atgtgtccag taaatgatcc ccttatcccg tcgcgatgct 50

4410> 36
 4411> 25
 4412> DNA
 4413> Artificial

4420>
 4421> Artificial sequence
 4422> 1-25
 4423> Synthetic construct.

4400> 36

<210> 35
<211> 37

<212> 37

<213> DNA

<214> Artificial

<215>

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<217> 1-23

<218> Synthetic construct.

<219> 37

<220> gagatccct aactatccag gag 23

<221> 38

<222> 39

<223> DNA

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<227> 1-39

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<229> 38

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<231> 39

<232> 40

<233> DNA

<234> Artificial

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<236> Artificial sequence

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<238> Synthetic construct.

<239> 40

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<241> 40

<242> 1084

<243> DNA

<244> Homo sapiens

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 35 40 45
 Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
 50 55 60
 Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
 65 70 75
 Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
 80 85 90
 Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
 95 100 105
 Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
 110 115 120
 Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
 125 130 135
 Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
 140 145 150
 Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
 155 160 165
 Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
 170 175 180
 Thr Tr Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
 185 190 195

Asp	Thr	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330

Arg Thr Ser Val

1110 - 42
 1111 - 1594
 1112 - DNA
 1113 - Homo sapiens

1100 - 41
 aacaggatct cctcttgcag tctgcagccc aggaagctga ttccagcaga 50
 gccttaacgc gcagcccga gattcaactat ggtgaaaato gccttcaata 100
 cccctaacgc cgtgcaaaag gaggaggcgc ggaagacgt ggaggccctc 150
 ctgagccgca cgttcagaac tcagatactg accggcaagg agctccgagt 200
 tgcaccccag gaaaaagagg gctcctctgg gagatgtatg cttaactctct 250
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 taaaagtact tcattgcctaa gagacccatt taccgtggag agatctgctt 350
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aaataata tatgatacct cttaataatt ctattgttat cctctcaaaa 600
 aatctggtag agctcttttg caaactggcg agtggcagat ctctgctca 650
 aatttatgtg gttcgagaag acctagttgc tctggaggaa attcgtgatg 700
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 agaagtcaga gatttacaat atactttta cattaagggt tatgggatac 950
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 ctctcttttt cctttaagta agctctttat ccatcttatg gtggagcaat 1250
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 ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
 aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500
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 cctataata aattttact tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 41

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
				20				25					30	
Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
				35				40					45	
Lys	Gln	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu

	40		50		60
Ser	Ile	Ile	Leu	Ala	Gly
	65				70
Leu	Ile	Val	Gly	Gly	Ala
					75
Cys	Ile	Tyr			
Lys	Tyr	Phe	Met	Pro	Lys
	80				85
Ser	Thr	Ile	Tyr	Arg	Gly
					90
Met	Cys				
Phe	Phe	Asp	Ser	Glu	Asp
	95				100
Pro	Ala	Asn	Ser	Leu	Arg
					105
Gly	Gly	Glu			
Pro	Asn	Phe	Leu	Pro	Val
	110				115
Thr	Glu	Glu	Ala	Asp	Ile
					120
Arg	Glu	Asp			
Asp	Asn	Ile	Ala	Ile	Ile
	125				130
Asp	Val	Pro	Val	Pro	Ser
					135
Phe	Ser	Asp			
Ser	Asp	Pro	Ala	Ala	Ile
	140				145
Ile	His	Asp	Phe	Glu	Lys
					150
Gly	Met	Thr			
Ala	Tyr	Leu	Asp	Leu	Leu
	155				160
Gly	Asn	Cys	Tyr	Leu	Met
					165
Pro	Leu	Phe			
Asn	Thr	Ser	Ile	Val	Met
	170				175
Pro	Pro	Lys	Asn	Leu	Val
					180
Glu	Leu	Phe			
Gly	Lys	Leu	Ala	Ser	Gly
	185				190
Arg	Tyr	Leu	Pro	Gln	Thr
					195
Tyr	Val	Val			
Arg	Glu	Asp	Leu	Val	Ala
	200				205
Glu	Glu	Ile	Arg	Asp	Val
					210
Ser	Asn				
Leu	Gly	Ile	Phe	Ile	Tyr
	215				220
Gln	Leu	Cys	Asn	Asn	Arg
					225
Lys	Ser	Phe			
Arg	Leu	Arg	Arg	Asp	Leu
	230				235
Leu	Leu	Gly	Phe	Asn	Lys
					240
Arg	Ala				
Ile	Asp	Lys	Cys	Trp	Lys
	245				250
Ile	Arg	His	Phe	Pro	Asn
					255
Glu	Phe	Ile			
Val	Glu	Thr	Lys	Ile	Cys
					260
Gln	Glu				

<210> 44

<211> 24

<212> DNA

<213> Artificial

<210>

<211> Artificial sequence

<212> 1-24

<213> Synthetic construct.

<400> 44

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<210> 45

<21> 21
LNA
<21> Artificial

<22> Artificial sequence
<22> 1-20
<22> Synthetic construct.

<400> 45
tttactgct atctgatgcc 20

<21> 46
<21> 26
<21> DNA
<21> Artificial

<220>
<22> Artificial sequence
<22> 1-26
<22> Synthetic construct.

<400> 46
tggatctcc tcttgcatgc tgcagc 26

<210> 47
<21> 28
<21> DNA
<21> Artificial

<220>
<22> Artificial sequence
<22> 1-28
<22> Synthetic construct.

<400> 47
ttctcgaac cacataagtt tgaggcag 28

<210> 48
<21> 25
<21> LNA
<21> Artificial

<220>
<22> Artificial sequence
<22> 1-25
<22> Synthetic construct.

<400> 48
tcaattccc tccatagaaa ctggcg 25

<210> 49
<21> 1969
<21> DNA
<21> Homo sapiens

<400> 49
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 cctcttgag aggcctgtgtt tctcgggaa tctcctctgg ggaagtcgga 1550
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 ggaataggt cctctccccc atcctctcat ctggggctcc cccaacctct 1750
 ctacagctct ccagtgctg agatattatg cactgcaca ataaaccttt 1800
 attcggcct gaaaaaaa aaaaaaaa aaaaaaaa aaaaaaaaaa 1850
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<210> 50
 <211> 283
 <212> FRT
 <213> Homo sapiens

<400> 50
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 20 25 30
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
 35 40 45
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
 65 70 75
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
 80 85 90
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
 95 100 105
 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
 110 115 120
 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
 125 130 135
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
 140 145 150
 Ser Thr Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Gln Gln Ala
 155 160 165

170 Arg Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr
 175
 180 Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp
 185
 190 Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys
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 200 Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro
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 210 Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
 215
 220 Gln Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly
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 230 Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro
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 240 Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val
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<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
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 gacccagagg gaggaggagc agggagtogg aagragagg acagajjagg 100
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 agaacctctg gagagagagg gggctgggca gagatgaagt tccaggggac 200
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 cctgcagaa cggagaggaa agcactggga caaatattgg ggagjccctt 300
 ggacatggcc tgggagagcc cctgagcgaa ggggtgggaa aggcattgg 350
 caagagagcc ggaggggag ctggctctaa agtcagtga ggccttggcc 400
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 acacacaa tactgtccgc gctctctggc agggggtgac tggccacagt 600
 attcttctt aaattcttgg aggcattgga atctttggct ctcaaggtgg 650
 ccttcttctt caattctt aaattctt aaattctt aaattctt aaattctt 700

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 ttttggaaa ttttggaaa ttttggaaa ttttggaaa ttttggaaa 1734

<110> 52
 <111> 440
 <112> PRT
 <113> Homo sapiens

<400> 1
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 1 5 10 15
 Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
 20 25 30
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
 35 40 45
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr	65	70	75
Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly	80	85	90
Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala	95	100	105
Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val	110	115	120
Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val	125	130	135
Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile	140	145	149
Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro	155	160	165
Gly	Gly	Leu	Gly	Thr	Pro	Trp	Val	His	Gly	Tyr	Pro	Gly	Asn	Ser	170	175	179
Ala	Gly	Ser	Phe	Gly	Met	Asn	Pro	Gln	Gly	Ala	Pro	Trp	Gly	Gln	185	190	195
Gly	Gly	Asn	Gly	Gly	Pro	Pro	Asn	Phe	Gly	Thr	Asn	Thr	Gln	Gly	200	205	210
Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Ser	Val	Arg	Ala	Ser	Asn	Gln	215	220	225
Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly	230	235	240
Ser	Ser	Asn	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gln	Ser	Gly	Ser	Ser	245	250	255
Gly	Ser	Gly	Ser	Asn	Gly	Asp	Asn	Asn	Asn	Gly	Ser	Ser	Ser	Gly	260	265	270
Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Gly	Ser	275	280	285
Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser	Gly	Asn	Ser	Gly	Gly	Ser	290	295	300
Arg	Gly	Asp	Ser	Gly	Ser	Gln	Ser	Ser	Trp	Gly	Ser	Ser	Thr	Gly	305	310	315
Ser	Ser	Ser	Gly	Asn	His	Gly	Gly	Ser	Gly	Gly	Gly	Asn	Gly	His	320	325	330
Lys	Leu	Gly	Cys	Gln	Lys	Leu	Gly	Asn	Gln	Ala	Arg	Gly	Ser	Gly	335	340	345

365 Gly Ile Glu Gly Ile Arg Gly Gly Gly Val Ser Ser Asn
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<210> 53
 <211> 3580
 <212> DNA
 <213> Homo sapiens

<400> 53
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 gtcacacag gtagaggaag gtagagacc gaccacata ttggagatat 750
 ctcttcca cctctgct ctccacacac agcattgac ctgggggagg 800

0010 = 10
0011 = 200
0012 = FRT
0014 = HIVE SATELLITE

400 34

Met	Cys	Ile	Leu	Asn	Lys	Leu	Leu	Leu	Leu	Ala	Val	Leu	Gly	Leu			
1				5						10							12
Leu	Ile	Gln	Ile	Pro	Thr	Val	Pro	Glu	Asp	Leu	Phe	Phe	Leu	Glu			
				20					25								30
Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Gln	Val	Asp	Thr	Val	Ala	Pro	Glu			
				35					40								45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr			
				50					55								60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser			
				65					70								75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys			
				80					85								90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln			
				95					100								105
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His			
				110					115								120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu			
				125					130								135
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val			
				140					145								150
Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu			
				155					160								165
Val	Thr	Gln	Gly	Gln	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu			
				170					175								180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala			
				185					190								195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg			
				200					205								210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala			
				215					220								225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp			
				230					235								240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala			
				245					250								255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala			
				260					265								270
Arg	Gly	Glu	Arg	Arg	Gly	Cys	Ser	Arg	Ala								
				275					28								

111 15
 112 2401
 113 1NA
 114 Brm. sapiens

1400 55
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 attctaat : agcatttg agagctatg tcttaata ggggtctct : 1300

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 a 2401

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 <212> PRT
 <213> Homo sapiens

<400> 56
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 45 46
 Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr Val Pro
 50 55 60
 Ile Leu Gly Asn Lys Thr Leu Pro Ser Arg Cys His Ala Cys Val
 65 70 75
 Ile Val Ser Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro
 80 85 90
 Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro
 95 100 105
 Thr Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg
 110 115 120
 Val Val Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln
 125 130 135
 Glu Ile Val Asn Arg Thr Pro Glu Thr Val Phe Ile Phe Trp Gly
 140 145 150
 Pro Pro Ser Lys Met Gln Lys Pro Gln Gly Ser Leu Val Arg Val
 155 160 165
 Ile Gln Arg Ala Gly Leu Val Phe Pro Asn Met Glu Ala Tyr Ala
 170 175 180
 Val Ser Pro Gly Arg Met Arg Gln Phe Asp Asp Leu Phe Arg Gly
 185 190 195
 Glu Thr Gly Lys Asp Arg Glu Lys Ser His Ser Trp Leu Ser Thr
 200 205 210
 Gly Trp Phe Thr Met Val Ile Ala Val Glu Leu Cys Asp His Val
 215 220 225
 His Val Tyr Gly Met Val Pro Pro Asn Tyr Cys Ser Gln Arg Pro
 230 235 240
 Arg Leu Gln Arg Met Pro Tyr His Tyr Tyr Glu Pro Lys Gly Pro
 245 250 255
 Asp Glu Cys Val Thr Tyr Ile Gln Asn Glu His Ser Arg Lys Gly
 260 265 270
 Asn His His Arg Phe Ile Thr Glu Lys Arg Val Phe Ser Ser Trp
 275 280 285
 Ala Gln Leu Tyr Gly Ile Thr Phe Ser His Pro Ser Trp Thr
 290 295

4210-32
 4211-4277
 4212-INA
 4213-Homo sapiens

400-50

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<210> 58
 <211> 1115

4117-15T
4118-Him sapiens

4200-58

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Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala
				20					25					30
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr
				35					40					45
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu
				50					55					60
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu
				65					70					75
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr
				80					85					90
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln
				95					100					105
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala
				110					115					120
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln
				125					130					135
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys
				140					145					150
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val
				155					160					165
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met
				170					175					180
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu
				185					190					195
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val
				200					205					210
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr
				215					220					225
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile
				230					235					240
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser
				245					250					255
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser
				260					265					270

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu	281	282	283
Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser	320	325	330
Glu Leu Val Ile Phe Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn Phe Pro Pro Ser Val Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala	365	370	375
Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Arg	410	415	420
Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys	545	550	555
Arg Gly Gln Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg			

	575	585	595
Arg Ile Lys Pro Glu Ile Met Ala Ser	Lys Glu Gln Gln Ile Gln		
575	585	595	
Arg Asp Asp Pro Gly Ala Ser Pro Gln	Ser Ser Ser Gln Pro Asp		
590	595	600	
Gly Arg Leu Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr Ile		
605	610	615	
Thr Thr Ala Ser Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro Arg		
620	625	630	
Gly Asn Gly Gly Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr Lys		
635	640	645	
Lys Leu Lys Lys Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala Ile		
650	655	660	
Pro Pro Ser Arg Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys Gly		
665	670	675	
Thr Ser Tyr Lys Phe Arg Val Arg Ala	Leu Asn Met Leu Gly Glu		
680	685	690	
Ser Glu Pro Ser Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly Tyr		
695	700	705	
Ser Gly Arg Val Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile Thr		
710	715	720	
Phe Thr Asp Ala Val Asn Glu Thr Thr	Ile Met Leu Lys Trp Met		
725	730	735	
Tyr Ile Pro Ala Ser Asn Asn Asn Thr	Pro Ile His Gly Phe Tyr		
740	745	750	
Ile Tyr Tyr Arg Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr Lys		
755	760	765	
Lys Asp Met Val Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser His		
770	775	780	
Leu Gln Pro Glu Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe Asn		
785	790	795	
Glu Gly Gly Glu Ser Glu Phe Ser Asn	Val Met Ile Cys Glu Thr		
800	805	810	
Lys Ala Arg Lys Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro Pro		
815	820	825	
Thr Leu Ala Pro Phe Gln Pro Pro Leu	Pro Glu Thr Ile Glu Arg		
830	835	840	
Pro Val Gly Thr Gly Ala Met Val Ala	Arg Ser Ser Asp Leu Pro		
845	850	855	

Leu	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	860	865	870
Val	Thr	Ile	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	875	880	885
Val	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	890	895	900
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	905	910	915
Ala	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	920	925	930
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	935	940	945
Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu	950	955	956
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His	965	970	975
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly	980	985	990
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro	995	1000	1005
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Gly	1010	1015	1020
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg	1025	1030	1035
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro	1040	1045	1050
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu	1055	1060	1065
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp	1070	1075	1080
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly	1085	1090	1095
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr	1100	1105	1110
Pro	Pro	Leu	Thr	Ile											1115		

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 1110 20
 1120 100
 1130 Artificial

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<123> Synthetic construct.

<400> 59
tttaattac gcaatcattg cctgc 25

<110> 60
<111> 24
<112> DNA
<113> Artificial

<120>
<121> Artificial sequence
<122> 1-24
<123> Synthetic construct.

<400> 60
tttaacgtag cctgtcgtg gagg 24

<110> 61
<111> 42
<112> DNA
<113> Artificial

<120>
<121> Artificial sequence
<122> 1-42
<123> Synthetic construct.

<400> 71
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<110> 62
<111> 1661
<112> DNA
<113> Homo sapiens

<120>
<121> unsure
<122> 678
<123> unknown base

<400> 62
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tgtgtgtctt gctactgttg ctgtctgtgc ggcagcncgt aaccgcgcgc 200
ggagccagcc cggggggccc cagagcccta tcaagatgg gctcccacag 250
cctttttacc ccggcgggtc tcccagngc cctcattacc ccaggcccca 300
tttggggggg tcccacaa aattggggtc ttgggtgtca cggcagacc 350

0016 - 68
 0017 - 469
 0018 - 117
 0019 - 117

100% pure
196, 306
unknown amino acid

4.1 (3)

Met Gln Pro Thr Gly Arg Glu Gly Ser Arg Ala Leu Ser Arg Arg
1 5 10 15

Tyr Leu Arg, Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg
20 25 30

His Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala
35 49 45

Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val
54 55 56

Pro Ser Ala Leu Thr Pro Gly Leu Thr Pro Gly Thr Pro
66 70 74

Iys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser

The Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg
49 100 100

Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg Asn Phe
110 115 120

Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val
 105 130 155

Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp
140 145 150

Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His
155 160 165

Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala
176 175 180

Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val
185 190 195

Xaa Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser
200 205 210

Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys
 .115 .120 .115

Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His Met
 130 135 140

Tyr	His	Asn	Val	Gly	Leu	Thr	Pro	Ile	Gly	Glu	Lys	Val	Val
445							250						255

Val. His Leu Arg Arg Leu Gly Met Met Ile Asp Leu Ser Tyr Ala

	277	285	290	295	300	305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	385	390	395	400	405	410	415	420	425	430	435	440	445	450	455	460	465	470	475	480	485							
Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro																																																	
Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu																																																	
Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly																																																	
Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu																																																	
Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg																																																	
Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp																																																	
Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr																																																	
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu																																																	
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg																																																	
Gln Val Glu Lys Val Arg Thr Glu Ser Arg Ala Gln Ser Pro Val																																																	
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser																																																	
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val																																																	
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala																																																	
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro																																																	
Thr Phe Thr Gln Trp Leu Cys																																																	

210-64

211-29

212-DNA

213-Artificial

220-

221-Artificial sequence

222-1-21

223-Synthetic construct.

4-14

<210> 1-25

<211> 15

<212> DNA

<213> Artificial

<210>

<211> Artificial sequence

<212> 1-25

<213> Synthetic construct.

<400> 65

atcacacaca gctctggaag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<210>

<211> Artificial sequence

<212> 1-47

<213> Synthetic construct.

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1364

<212> DNA

<213> Homo sapiens

<400> 67

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ggcccagaaa gcttgataag catgaagctc ttatcttttg tggtgtgtgt 150
cgggtgtttg ctggtgcacc cagatgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcactgtt ccacttata gaaacatcag tgggcacatt 250
tacaacacaa atgtatcaca gaaggactgc aactgcctgc acgtggtgga 300
gcccattgca gtccctgcac atgacgtgga ggccactgc ctgctgtgcg 350
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gttccttgac cctctcactc gaaagcccca tgcatacact gacaaactgc 500
tgcctaggga agaaatcag gatgctggt ctatggcacc agtcgctgaa 550
tgcctagaa cagctcagg aaacacatc ctgagctgt tgaacatc 600

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 25 50
 Tyr Glu Tyr Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
 75 100
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
 125 150
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
 175 200
 Ala Tyr Thr Glu Glu Leu His Asn Glu Glu Glu Asn Glu Asp Ala
 225 250
 Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
 275 300
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
 325 350
 Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
 375 400
 Met Leu Ser

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
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 tccctttgca ttcacccc tccgggttt gcttctctc ggggaacccc 200
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 ggggaactaa gaaggacaaa aactggggg aggcctaccc ttgtagcagt 450
 cataaggagt gtgaagttag gaggtatt ccacactccc accaagcatt 500
 atcggtctg atctctgt ggacaaaaa gaagcctgc caccgagatg 550
 gcatctata cccactac ccttcaata atgctatc tatccagtt 600
 actgaacaa tcttctct tctctctc atctggag ctacttgg 650

Thr Pro Gly His Ala Ala Asn Arg Ser Ala Gly Met Tyr His Gly
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 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly His Ala
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 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
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 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
 45 50 55 60
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
 65 70 75 80 85
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
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 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
 110 115 120 125
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
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 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
 155 160 165 170 175
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
 180 185 190 195 200
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
 205 210 215 220 225
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
 230 235 240 245 250
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 255 260 265 270 275
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
 280 285 290 295 300

Cys Gln Lys Ile

<110> 71

<111> 1809

<112> DNA

<113> Homo sapiens

<400> 71

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gaatcaggtt tttaaaaaatt gattttctta aattatggc caattattgg 150

cttctctta gattttatg tttttcag gaaggtatg tttttttt 200

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Ser	Ser	Gln	Asn	Ser	Asn	Gln	Ile	Ile	Ser	Leu	Tyr	Ser	Lys	
				239				244					249	
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245				250						255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260				265						270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275				280						285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290				295						300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305				310						315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320				325						330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335				340						345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
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Ser Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<214>
 <215> Artificial sequence
 <216> 1-26
 <217> Synthetic construct.

<218> 73
 <219> attcatggc aaatatttcc ctcccc 26

<220> 74
 <221> 22
 <222> DNA
 <223> Artificial

<224>
 <225> Artificial sequence
 <226> 1-22
 <227> Synthetic construct.

<228> 74
 <229> tgcataaact tgcataaact gc 22

<230> 75
 <231> 56

<110> RNA
<111> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
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<110> 76
<111> 1989
<112> DNA
<113> Homo sapiens

<400> 76
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tgcactcagg ggtggaggag acggacggcg gctgtacac ctgcacacctg 150
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<110> 77
 <111> 341
 <112> PRT
 <113> Homo sapiens

<400> 77
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 35 40 45
 Tyr Gln Ser Leu Ala Val Arg Leu Gln Val Thr Asp Gly Pro Pro
 50 55 60
 Ala Thr Pro Ala Tyr Trp Asp Gly Gln Lys Gln Val Leu Ala Val
 65 70 75

Ala Arg Gly Ala 1:	Ala Leu Leu Thr	Tyr Val Asn Arg	Gly His
50		85	20
Val Trp Thr Asp Arg	His Val Glu Glu	Ala Gln Phe Val	Val His
95		130	105
Trp Asp Arg Gln Pro	Pro Gly Val Pro	His Asp Arg Ala	Asp Arg
110		115	100
Leu Leu Asp Leu Tyr	Ala Ser Gly Glu	Arg Arg Ala Tyr	Gly Pro
125		135	135
Leu Phe Leu Arg Asp	Arg Val Ala Val	Gly Ala Asp Ala	Phe Glu
140		145	150
Arg Gly Asp Phe Ser	Leu Arg Ile Glu	Pro Leu Glu Val	Ala Asp
155		160	165
Glu Gly Thr Tyr Ser	Cys His Leu His	His His Tyr Cys	Gly Leu
170		175	180
His Glu Arg Arg Val	Phe His Leu Thr	Val Ala Glu Pro	His Ala
185		190	195
Glu Pro Pro Pro Arg	Gly Ser Pro Gly	Asn Gly Ser Ser	His Ser
200		205	210
Gly Ala Pro Gly Pro	Asp Pro Thr Leu	Ala Arg Gly His	Asn Val
215		220	225
Ile Asn Val Ile Val	Pro Glu Ser Arg	Ala His Phe Phe	Gln Gln
230		235	240
Leu Gly Tyr Val Leu	Ala Thr Leu Leu	Leu Phe Ile Leu	Leu Leu
245		250	255
Val Thr Val Leu Leu	Ala Ala Arg Arg	Arg Arg Gly Gly	Tyr Glu
260		265	270
Tyr Ser Asp Gln Lys	Ser Gly Lys Ser	Lys Gly Lys Asp	Val Asn
275		280	285
Leu Ala Glu Phe Ala	Val Ala Ala Gly	Asp Gln Met Leu	Tyr Arg
290		295	300
Ser Glu Asp Ile Gln	Leu Asp Tyr Lys	Asn Asn Ile Leu	Lys Glu
305		310	315
Arg Ala Glu Leu Ala	His Ser Pro Leu	Pro Ala Lys Tyr	Ile Asp
320		325	330
Leu Asp Lys Gly Phe	Arg Lys Glu Asn	Cys Lys	
335		340	

2200> 78
 2211> 224
 2212> ENA
 2213> Homo sapiens

400-7A

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 <211> 475
 <212> PRT
 <213> Homo sapiens

<400> 79
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 Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
 35 40 45
 Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
 50 55 60
 Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
 65 70 75
 Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
 80 85 90
 Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
 95 100 105

Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Ile	Ser	Met	Leu	Cys	Leu	Val	111	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Ile	Gly	Ile	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Ile	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

	395	400	405
Leu Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser			
	410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu			
	425	430	435
Thr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly			
	440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser			
	455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu Ile			
	470	475	

<2100> 30
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 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<230> 40
 <231> ggttggtc accattgtct gc 22

<240> 31
 <241> 1-3
 <242> DNA
 <243> Homo sapiens

<250>
 <251> Artificial sequence
 <252> 1-23
 <253> Synthetic construct.

<260> 21
 <261> gtagtgac acagaagccc agg 23

<2700> 32
 <2710> 49
 <2720> DNA
 <2730> Artificial

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 <2710> Artificial sequence
 <2720> 1-49
 <2730> Synthetic construct.

<280> 62
 <281> atgtgatga ccagttcttt tttatataagg aaattccagat cactgatat 49

<2900> 43
 <2910> 1-44

1.1.1 DNA
1.1.2 Homo sapiens

400 bases

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 cctctgtctt cgtcccccac cctctcagcc tggctggctc ccaggactgg 150
 aagcctgaac gcagccaga ccccttcagc aattgcctgc aggatcctca 200
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 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
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 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
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 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
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 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
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 Gln Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
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245	Leu Ser Phe Ala Glu Ala Leu Arg Ala	His Ser Cys Leu Ser Asp	245
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275	Arg Ala Leu Leu Ser Ser Leu Ser Gly	Leu Val Leu Leu Asn Ala	275
290	Pro Val Val Ala Met Thr Gln Gly Pro	His Asp Val His Val Gln	290
305	Ile Glu Thr Ser Pro Pro Ala Arg Asn	Leu Lys Val Leu Lys Ala	305
320	Asp Val Val Leu Leu Thr Ala Ser Gly	Pro Ala Val Lys Arg Ile	320
335	Thr Phe Ser Pro Pro Leu Pro Arg His	Met Gln Glu Ala Leu Arg	335
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365	Arg Pro Phe Trp Arg Glu Glu His Ile	Glu Gly Gly His Ser Asn	365
380	Thr Asp Arg Pro Ser Arg Met Ile Phe	Tyr Pro Pro Pro Arg Glu	380
395	Gly Ala Leu Leu Leu Ala Ser Tyr Thr	Trp Ser Asp Ala Ala Ala	395
410	Ala Phe Ala Gly Leu Ser Arg Glu Glu	Ala Leu Arg Leu Ala Leu	410
425	Asp Asp Val Ala Ala Leu His Gly Pro	Val Val Arg Gln Leu Trp	425
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His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Pro Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Glu Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
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Phe	Asn	Phe	Leu	Ile	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile
									70				71
Ile	Leu	Thr	Ile	Gly	Ala	Ala	Ile	Phe	Ileu	Trp	Leu	Ile	Thr
									85				90
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser
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Met	Ile	Gln	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn
									115				120
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr
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Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys
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Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr
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Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu
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Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe
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Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr
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Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro
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Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val
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Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val
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Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp
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Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile
									280				285
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Gln	Asn	Leu	Gly	Lys	Glu	His
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Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Gln	Asp	Leu	Ser	Val	Ile
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													Thr

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His Ala Tyr Glu Phe	Thr Pro Asp Asp Val Ala Ile Ser Tyr	
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Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
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Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
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Leu Leu Ala Asp Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe Pro	
410	415	420
Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
425	430	435
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
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Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
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Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
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590	595	600
Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
605	610	615
Phe Lys Leu Ala Gln Gly Gln Tyr Ile	Ala Pro Gln Lys Ile Glu	

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
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									640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
									655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
									670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
									685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
									700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
									715					720
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His Ile Gln Asp														

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- 2.10. 88
- 2.11. 660
- 2.12. 58T
- 2.13. Homo sapiens

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				20					25					30	
Asn	Gln	Arg	Ala	Leu	Arg	Arg	Phe	Cys	Gln	Thr	Gly	Ala	Val	Leu	
				35					40					45	
Phe	Leu	Leu	Val	Thr	Val	Ile	Val	Asn	Ile	Lys	Leu	Ile	Leu	Asp	
				50					55					60	
Thr	Arg	Arg	Ala	Ile	Ser	Glu	Ala	Asn	Glu	Asp	Pro	Glu	Pro	Glu	
				65					70					75	
Gln	Asp	Tyr	Asp	Glu	Ala	Leu	Gly	Arg	Leu	Gln	Pro	Pro	Arg	Arg	
				80					85					90	
Arg	Gly	Ser	Gly	Pro	Arg	Arg	Val	Leu	Asp	Val	Glu	Val	Tyr	Ser	
				95					100					105	
Ser	Arg	Ser	Lys	Val	Tyr	Val	Ala	Val	Asp	Gly	Thr	Thr	Val	Leu	
				110					115					120	
Gln	Asp	Glu	Ala	Arg	Glu	Gln	Gly	Arg	Gly	Ile	Ser	Val	Ile	Val	
				125					130					135	

Asn	Ala	Thr	Gly	His	Val	Met	Ala	Lys	Arg	Val	Phe	Arg
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Thr	Tyr	Ser	Trp	His	Gln	Asp	Gln	Ala	Met	Val	Leu	Phe
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Met	Val	Ala	Pro	Gly	Arg	Val	Leu	Ile	Lys	Thr	Val	Lys
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Gly	Ser	Phe	His	Leu	Lys	Asp	Thr	Ala	Lys	Ala	Leu	Leu
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Leu	Gly	Ser	Gln	Ala	Gly	Pro	Ala	Leu	Gly	Tyr	Arg	Asp
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Ala	Phe	Val	Gly	Arg	Lys	Gly	Gly	Pro	Val	Phe	Gly	Glu
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Ser	Lys	Ser	Pro	Ala	Leu	Ser	Ser	Trp	Gly	Asp	Pro	Val
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Lys	Thr	Asp	Val	Pro	Leu	Ser	Ser	Ala	Glu	Glu	Ala	Glu
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Trp	Ala	Asp	Thr	Glu	Leu	Asn	Arg	Arg	Arg	Arg	Phe	Cys
				260					265			270
Lys	Val	Glu	Gly	Tyr	Gly	Ser	Val	Cys	Ser	Cys	Lys	Asp
				275					280			285
Pro	Ile	Glu	Phe	Ser	Pro	Asp	Pro	Leu	Pro	Asp	Asn	Lys
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Asn	Val	Pro	Val	Ala	Val	Ile	Ala	Gly	Asn	Arg	Pro	Asn
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Tyr	Arg	Met	Leu	Arg	Ser	Leu	Leu	Ser	Ala	Gln	Gly	Val
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Gln	Met	Ile	Thr	Val	Phe	Ile	Asp	Gly	Tyr	Tyr	Glu	Glu
				335					340			345
Asp	Val	Val	Ala	Leu	Phe	Gly	Leu	Arg	Gly	Ile	Gln	His
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Ile	Ser	Ile	Lys	Asn	Ala	Arg	Val	Ser	Gln	His	Tyr	Lys
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Leu	Thr	Ala	Thr	Phe	Asn	Leu	Phe	Pro	Glu	Ala	Lys	Phe
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Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe
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Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Gln	Glu	Asp	Asp	Ser
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Tyr	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Ala	His	Thr

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Met Pro Glu Gln Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val		
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Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly		
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Tyr Phe His Glu Arg Tyr Phe Lys Lys His Lys Phe Asn Thr Val		
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Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala		
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Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr		
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Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp		
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp		
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Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe		
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro		
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35 40 45
Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
50 55 60
Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
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Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
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Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
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Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
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Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
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Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
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Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
170 175 180
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Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
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Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
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Tyr Leu Gly Leu Ser Lys Ser Ser Lys Ala Ala Leu Ser Gln Val

	230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu	245	250	255
Iyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly	260	265	270
His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg	275	280	285
Leu Glu Val Ala Ala Leu Val Leu Gly Cys Leu Ile Pro Leu Ile	290	295	300
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THE FUTURE

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<213> Homo sapiens

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Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
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Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
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Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
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Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
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Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
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Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
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Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
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Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
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Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
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Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
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Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
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Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
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Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
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Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
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Ala	Val	Val	Leu	Asp	Ser	Lys	Arg	Gln	Val	Glu	Lys	Gln	Gln	Thr	245	250	255
Arg	Glu	Ile	Gln	Val	Val	Asn	Glu	Glu	Pro	Gln	Arg	Asp	Arg	Leu	260	265	270
Ile	Gln	Glu	Pro	Gly	Arg	Glu	Gln	Val	Val	Glu	Asp	Arg	Pro	Val	275	280	285
Gly	Gly	Arg	Gly	Phe	Gly	Gly	Ala	Gly	Glu	Leu	Gly	Gln	Thr	Pro	290	295	300
Gln	Val	Gln	Ala	Ala	Leu	Ser	Val	Ser	Gln	Glu	Asn	Pro	Glu	Met	305	310	315
Glu	Gly	Pro	Glu	Arg	Asp	Gln	Leu	Val	Ile	Pro	Asp	Gly	Gln	Glu	320	325	330
Glu	Glu	Gln	Glu	Ala	Ala	Gly	Glu	Gly	Arg	Asn	Gln	Gln	Lys	Leu	335	340	345
Arg	Gly	Glu	Asp	Asp	Tyr	Asn	Met	Asp	Glu	Asn	Glu	Ala	Glu	Ser	350	355	360
Glu	Thr	Asp	Lys	Gln	Ala	Ala	Leu	Ala	Gly	Asn	Asp	Arg	Asn	Ile	365	370	375
Asp	Val	Phe	Asn	Val	Glu	Asp	Gln	Lys	Arg	Asp	Thr	Ile	Asn	Leu	380	385	390
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 211-PRT
 111-Hom sapiens

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 Gly Pro Gly Ser Leu Pro Trp Gly Ser Glu Gly Lys Pro Gly Ala
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 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
 65 70 75
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 80 85 90
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
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 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
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 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
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 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
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215	215	225	
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Gly Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln Met	245
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Ser Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp Thr	260
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Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly Asp	275
275	280	285	
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe Leu	290
290	295	300	
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu Pro	305
305	310	315	
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu Leu	320
320	325	330	
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met Ala	335
335	340	345	
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser Ala	350
350	355	360	
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val Ser	365
365	370	375	
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln Ala	380
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Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser Ala	395
395	400	405	
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala Thr	410
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Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly Ala	425
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455	460	465	
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe Cys	470
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Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala Ile	485
485	490	495	

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Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met
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Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala
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Val	Ser	Gly	Ala	Ser	Met	Val	Leu	Pro	Arg	Ala	Val	Ala	Gly	Leu
740									745					750
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755									760					765
Leu	Val	Lys	Ala	Gly	Ala	Gly	Ala	Pro	Arg	Thr	Arg	Thr	Val	Leu
770									775					780
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783	786	789
Val Val Ile Gln Ile Tyr Arg His Met	Gln Glu Glu Phe Arg Gly	800
Arg Leu Glu Arg Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala	815
Gln Glu Leu Gly Ser Val Tyr Ser Ala	Ala Met Val Thr Ala Leu	830
Val Leu Leu Ala Phe Pro Leu Leu Leu	Leu His Ala Glu Arg Ile	845
Ser Leu Val Phe Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu Leu	860
His Leu Leu Ala Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro Phe	875
Thr Val Pro Trp Gln Ala Val Ser Ala	Trp Ala Leu Met Ala Thr	890
Gln Thr Phe Tyr Ser Thr Gly His Gln	Pro Val Phe Pro Ala Ile	905
His Trp His Ala Ala Phe Val Gly Phe	Pro Glu Gly His Gly Ser	920
Cys Thr Trp Leu Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe Ala	935
Ser His Leu Leu Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu Trp	950
Pro Phe Leu Cys Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro	965
Pro Gly Asn Glu Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu Glu	980
Glu Pro Leu Met Glu Met Arg Leu Arg	Asp Ala Pro Gln His Phe	995
Tyr Ala Ala Leu Leu Gln Leu Gly Leu	Lys Tyr Leu Phe Ile Leu	1010
Gly Ile Gln Ile Leu Ala Cys Ala Leu	Ala Ala Ser Ile Leu Arg	1025
Arg His Leu Met Val Trp Lys Val Phe	Ala Pro Lys Phe Ile Phe	1040
Glu Ala Val Gly Phe Ile Val Ser Ser	Val Gly Leu Leu Leu Gly	1055
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<212> DNA
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<223> Synthetic construct.

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<223> Synthetic construct.

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<121> 1-51
<122> Synthetic construct.

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<112> DNA
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Proteinase 1114

210 - 111

211 - 283

212 - PPT

213 - Homo sapiens

400 - 111

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Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
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Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
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Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
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His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
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Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
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Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
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Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
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Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Glu	Val	Ser	Ala	Phe	Val
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<210>
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<213> Synthetic construct.

<210> 113
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<210>
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<213> Synthetic construct.

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<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

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 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
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 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Ile Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
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 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
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Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro	
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Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro	
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Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly	
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Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala	
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Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg	
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Gly	Asn	Val	Ser	Cys	Ala	Leu	Ser	Leu	Ser	Arg	Ala	Phe	Leu	Leu	245	250	255
Tyr	Ser	Pro	Asp	Asn	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr	260	265	270
Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala	275	280	285
Val	Ile	Gln	Arg	Pro	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr	290	295	300
Tyr	Glu	Gly	Leu	Cys	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr	305	310	315
Gln	Ile	Pro	Ser	Leu	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala	320	325	330
Tyr	Leu	Leu	Leu	Gln	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu	335	340	345
Pro	Tyr	Ile	Ala	Leu	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala	350	355	360
Gln	Lys	Ile	Arg	Glu	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val	365	370	375
Val	Ala	Ser	Gly	Glu	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser	380	385	390
Lys	Ser	Ala	Trp	Leu	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr	395	400	405
Leu	Asn	His	Arg	Ile	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro	410	415	420
Pro	Tyr	Ala	Glu	Tyr	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly	425	430	435
His	Tyr	Glu	Pro	His	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro	440	445	450
Leu	Tyr	Arg	Met	Lys	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile	455	460	465
Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	470	475	480
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	485	490	495
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	500	505	510
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	515	520	525
Trp	Ile	His	Gln	Tyr	Gly	Gln	Gln	Phe	Arg	Arg	Pro	Cys	Ser	Ser			

Ser Pro Glu Asp

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<218> 23

<218> DNA

<218> Artificial

<220>

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<220> 1-23

<220> Synthetic construct.

<220> 119

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<210> 120

<210> 24

<210> DNA

<210> Artificial

<220>

<220> Artificial Sequence

<220> 1-24

<220> Synthetic construct.

<220> 120

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<210> 121

<210> 49

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<210> Artificial

<220>

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<220> 1-49

<220> Synthetic construct.

<220> 121

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<210> 1778

<210> DNA

<210> Homo sapiens

<210> 122

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gaatgacac tgcacgttg gacacagac gctgggtgag ggaacacac 150

gaatgacac tgcacgttg gacacagac gctgggtgag ggaacacac 200

atgagttttt tgggtttttt tttttttttt tttttttttt tttttttttt 177

ttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 178

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<211> 294

<212> HAT

<213> Homo sapiens

<400> 123

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35 40 45

Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
50 55 60

Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
65 70 75

Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
80 85 90

Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
95 100 105

Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
110 115 120

Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
125 130 135

Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
140 145 150

Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
155 160 165

Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
170 175 180

Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
185 190 195

Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
200 205 210

Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
215 220 225

Trp Phe Met Asp Asp Tyr Thr Ile Met Ala Lys Ile Leu Leu Gly

	137	138	139
Ile Leu Leu Pro Gln Phe Leu Gly Val Leu Leu Thr Leu Leu Tyr	243	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met Glu His Ser Val Thr Asp	260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro Ser Val Glu Ala Ala Gly	275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn	290		

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 <212> DNA
 <213> Artificial

<220>
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 <222> 1-25
 <223> Synthetic construct.

<400> 124
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<210> 115
 <211> 25
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-25
 <223> Synthetic construct.

<400> 115
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<210> 116
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 116
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<210> 127
 <211> 1636
 <212> RNA
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491 127

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332 335 340

Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
345 350 355

Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
360 365 370

Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
375 380 385

Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
390 395 400

Ile Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
405 410 415

Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
420 425 430

Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
435 440 445

Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
445 450 455

Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
455 460 465

Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
470 475 480

Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
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Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
500 505 510

Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
515 520 525

Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
530 535 540

Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
545 550 555

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
555 560 565

Pro Val Ser Gln

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- * 211 - 221
- * 212 - DNA
- * 213 - Homo sapiens

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11 115 120

Ile Asp Gln Gly Ser Asp Val Ile Gln Met Leu Asn Met Asn Ser
121 130 135

Ala Leu Thr Ile Ile Asn Ile Pro Ala Lys Gly Lys Pro Lys Arg
140 145 150

Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln
151 160 165

Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val
170 175 180

Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu
181 190 195

Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met
200 205 210

Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys
211 220 225

Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
230 235 240

Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn
241 250 255

Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His
260 265 270

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271 280 285

Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys
290 295 300

Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser
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320 325 330

Ser Ile Leu Met Ser
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<212> PNA

<213> Homo sapiens

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carboxyl-terminal fragment of the protein of the

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 acctgtaat ccaaaacttt gggaactga ggaagcaga tcacaaggta 1900
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 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
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Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
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Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
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His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145						150
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
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Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
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Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
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Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205						210
Pro	Ser	Irc	Ser	Ser	Gly	Gln	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220						225
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235						240
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250						255
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265						270
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280						285
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295						300
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310						315
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
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Glu	Ala	Ser	Ala	His	Val	Irc	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
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Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
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Leu	Ser	Gly	Tyr	Ser	Leu	Leu	Pro	Leu	Ser	Ser	Gln	Thr	Phe	Lys
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Asn	Gln	His	Lys	Val	Lys	Asn	Leu	His	Pro	Pro	Trp	Ile	Leu	Ser
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Glu	Phe	His	Gly	Cys	Asn	Val	Asn	Ala	Ser	Thr	Tyr	Met	Leu	Arg
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Thr	Asn	His	Trp	Lys	Tyr	Ile	Ala	Tyr	Ser	Asp	Gly	Ala	Ser	Ile
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Leu	Pro	Gln	Leu	Phe	Asp	Leu	Ser	Ser	Asp	Pro	Asp	Glu	Leu	Thr
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Asn	Val	Ala	Val	Lys	Phe	Pro	Glu	Ile	Thr	Tyr	Ser	Leu	Asp	Gln
				455					460					465
Lys	Leu	His	Ser	Ile	Ile	Asn	Tyr	Pro	Lys	Val	Ser	Ala	Ser	Val
				470					475					480
His	Gln	Tyr	Asn	Lys	Glu	Gln	Phe	Ile	Lys	Trp	Lys	Gln	Ser	Ile
				485					490					495
Gly	Gln	Asn	Tyr	Ser	Asn	Val	Ile	Ala	Asn	Leu	Arg	Trp	His	Gln
				500					505					510
Asp	Trp	Gln	Lys	Glu	Pro	Arg	Lys	Tyr	Glu	Asn	Ala	Ile	Asp	Gln
				515					520					525
Trp	Leu	Lys	Thr	His	Met	Asn	Pro	Arg	Ala	Val				
				530					535					

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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 gcttctactg agaggtctgc catggcctct cttagcctcc aatttgtgg 150
 ctatgctcga ggccttctcg ggccttttggg cactctggtt gccatgctgc 200
 tcccagctc gaaaacaagt tcttatctcg gtgcagcat tctgacagca 250
 cttagcttct caaagggcct ctggatgaa tctacacac atagacagca 300
 atcacacac tctgacatct atagcagcct tctgagctc agcctgaca 350
 tccaggcttc caagggaatg atgctgacat caattgcat ctctgctct 400
 ctctgctct tctctgtgtt aggtatata tgcacatct tctctctga 450

atcagggat aagacagac tggcgtatc atcagcgc tttttcatt 15
 ttggagagct cctgggattc attcctattc cctaaatct tcatgggata 50
 ctacaggact tctactcacc actgatgact tacagcatca atttgagat 60
 tggagaggct atttacttgg gatttatctc t'cctatctc tccctgatag 65
 ctgaaatcat cctctgcttt tctctctat cccagagaaa tggctccaa 70
 tactaagatc cttacaaagc caaacctctt ggcacaagga cctctcvaag 75
 ggcctggcaca cctcccaag taaagagtga attcaattcc tacagcctga 80
 cagggtatgt gtgaagaacc aggggcaca cctagggagt ggcctggatct 85
 gtgaanaaca gtggacagca ccccgaggcc cacaggtcag ggacactcc 90
 atgggacgtt gtcagaaggt gctgctgacc ataaactgac tttgctcatt 95
 ggaatgagca aaggcagaaa tgggggctag tctaacagca tgcaggttga 100
 attgcacaag atgctcgaca tgcagcctt tctttttcc tcaacttgc 105
 gctccctgc cttaaqtccc caacctcaa cttgaaaccc cattcctta 110
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 ccccaaccc actaatcaca tccctctgac taactcttg tgaacaaaga 120
 cccctctct gctgaggtt ggcctttacc tcaattgctgg gcatgggaag 125
 gagaagcagt ggcctttgtg ggcattgctc taacctactt ctcaagcttc 130
 cctccaaaga aactgatttg cccctggaac tccatccac tcttgttatg 135
 actccacagt gtcacagact atttgtgcat caactgaat aaaaccatcc 140
 taugtatcc agggaacaga aagcaggatg caggatggga qgacagggaag 145
 gcaqccctggg acatttaaaa aaata 1475

<210> 134

<211> 230

<212> FET

<213> Homo sapiens

<200> 134

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 1 5 10 15

Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Phe Ser Trp
 20 25 30

Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
 35 40 45

Ile Ser Lys Gly Leu Trp Met Gln Tyr Ala Thr His Ser Thr Gly

Ile Thr Gln Cys Asp	Ile Tyr Ser Thr	Leu Leu Gly Leu Ile	Ala
65			75
Asp Ile Gln Ala Ala	Gln Ala Met Met	Val Thr Ser Ser	Ala Ile
80		85	90
Ser Ser Leu Ala Cys	Ile Ile Ser Val	Val Gly Met Asn	Cys Thr
95		100	105
Val Phe Cys Gln Glu	Ser Arg Ala Lys	Asp Arg Val Ala	Val Ala
110		115	120
Gly Gly Val Phe Phe	Ile Leu Gly Gly	Leu Leu Gly Phe	Ile Pro
125		130	135
Val Ala Trp Asn Leu	His Gly Ile Leu	Arg Asp Phe Tyr	Ser Pro
140		145	150
Leu Val Pro Asp Ser	Met Lys Phe Glu	Ile Gly Glu Ala	Leu Tyr
155		160	165
Leu Gly Ile Ile Ser	Ser Ser Leu Phe	Ser Leu Ile Ala	Gly Ile Ile
170		175	180
Leu Cys Phe Ser Cys	Ser Ser Gln Arg	Asn Arg Ser Asn	Tyr Tyr
185		190	195
Asp Ala Tyr Gln Ala	Gln Pro Leu Ala	Thr Arg Ser Ser	Pro Arg
200		205	210
Pro Gly Gln Pro Pro	Lys Val Lys Ser	Glu Phe Asn Ser	Tyr Ser
215		220	225
Leu Thr Gly Tyr Val			
230			

<210> 135

<211> 610

<212> DNA

<213> Homo sapiens

<400> 135

gcactgctgc tgtcccatca gctgctctga agctccatgg tgcccagaat 50

cttcgctcct acttatgtgt cagtctgtct cctctctttg tgtccaaggg 100

aagtcacggc tcccgttggc tcagaacctt ggcctgtgcca gccgcacch 150

agctgtggag acaagatcta caaccctttg gaggactgct gttacaatga 200

agccatggtg tccctagagg aacccggcca atctgtgtcc ccttcacact 250

tctggacctg cttttagctc tctctctttg attcctttg ccttcacaaa 300

acttctcttg tcaactgaa gttccacttt ctactctccc attgcactg 350

atctccatc ttagagaaat agaaagag agaaagtttt ccttgagaa 400
 aatagaaaag aaaatcaat ttcaataagg catctcaga acataggcta 450
 aggtaatatg tgtacagta agaaagcctg aggaattttac aaatgata 500
 agctccaagc cattgtatgg cccatgtggg agaactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggttttt caatgtacac 600
 aactgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
 1 5 10 15
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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 gtcttttgcca tttttctgat ctccagggctc ctctgtctac acgagacccc 100
 agtggccccc atgaactcctt acctaatgct gtgcacagcca caaagagat 150
 atgggaaaaa gttctacagac cccctcagc actgtttgcta tgat atgac 200
 ctcttgact tccctaggac ccagacattat agaaactgta cctttagat 250

ctactttgag ctatgatac cctgactt catatgaa ctataacc 390
 aqaactggga ctacgacggg acctcagatg acaggctttg tacaactata 395
 agtlaaatgga acatcagggg aacgatgaat cctggattct ctttcttggg 400
 tgggcctgga gaaagagggt ggtgttaact gagatctagg atgttgggtg 450
 gctgttttggg ggcacagaga aacacacact aactaccac ttctattctgt 500
 gacctgtctg aggcacacac tgcagctgac ctgaggagge acacagatcc 550
 cctttctagaa ttctggacag catgagatgc gtgtgtgtgat ggggggcacg 600
 ggctctgaa cctctctgat aacctctatg gcaacatca acccggaacc 650
 acaccaagge tggttgggga accttcaac cttctgtgac attttctatc 700
 atctcaagtt ctctttctatc caggagcaaa gcacaggatc ataataaatt 750
 tatgtacttt ataaatgaaa a 771

<210> 138
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 138
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 Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met
 20 25 30
 Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
 35 40 45
 Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
 50 55 60
 Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
 65 70 75
 Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
 80 85 90
 Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
 95 100 105
 Cys Arg Ser Val Ser
 110

<210> 139
 <211> 2044
 <212> DNA
 <213> Homo sapiens

<400> 139

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 gctgggactc agtggggga ggttggggg gggggggg gttggggg 100
 ctgggggga cgggaagttc ctggggggg gggggggg cgtggggg 150
 cggggggg tggggggg ggttggggg tggggggg tggggggg 200
 tcttttctg gctgggttc taggtgggt gggggggtc aagggtggc 250
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 tgggggtct tgggggtgt ggggaagg cgggtgta cttttttaa 350
 ggttgggtc gggggggg gggggggg gggggggg tggggggg 400
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 cggggggg gggggggg gggggggg gggggggg gggggggg 500
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 gggggggg gggggggg gggggggg gggggggg gggggggg 1050
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 gggggggg gggggggg gggggggg gggggggg gggggggg 1400
 gggggggg gggggggg gggggggg gggggggg gggggggg 1450

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0210 · 140
0211 · 311
0212 · FRT
0213 · Homo sapiens

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Met	Gly	Val	Pro	Thr	Ala	Leu	Gln	Ala	Gly	Ser	Trp	Arg	Trp	Gly	15
1				5					10					15	
Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	30
				20					25					30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	45
				35					40					45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	60
				50					55					60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	75
				65					70					75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	90
				80					85					90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	105
				95					100					105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	120
				110					115					120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	135
				125					130					135	
Leu	Thr	Leu	Leu	Asp	Phe	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Gln	150

147	148	149
Ile Arg His His His Ser Gln His Arg Val His Gly Ala Met Gln		
155	160	165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val		
170	175	180
Tyr Pro Ser Ser Ser Gln Asp Ser Gln Asn Ile Thr Ala Ala Ala		
185	190	195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu		
200	205	210
Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg		
215	220	225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile		
230	235	240
Gln Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro		
245	250	255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln		
260	265	270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro		
275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp		
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile		
305	310	

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 tttagacctc cttctctgcc ctcttttctt gacacacgtt ccttcctggc 150
 ccttctccga ccccgctctt gccacagacc tactgggctc tgtgggttga 200
 tctgtggccc ctgtgctctc gttctctttt cgtcttcctt ccttcacgac 250
 ccgctccggg accagcgccc tgaccttggg gaaaggatgg ttcccgaggt 300
 gaaggctctc tctctcttcc tgggaactcc gctgctatgg ttccctctag 350
 actccacatc tccagccccc ccagacatc tcttctttt ccatgaccaa 400
 agtacttc cccacagacg ctccacaccc tacttggagg cacaacacct 450

atctataga ctgggttgta atgtctaga ggcacccat gtgattgtt 500
 atggaatcca atgtctgctt gtcactcc: cccagcctgt gaaggatcca 550
 caggaaatct gtcccaagtg tctggaacct cacaactccct ctggaaatccg 600
 rccccaaca aagtcctgac agcacaaagg caccatgtac caacacggat 650
 aatctcttag tgcacatgag ctgttccct cctgctgac caacacatct 700
 gtccctatga gctgacaga tggccagatc tattgaggcc tcacaaatct 750
 cccgaagca ggtctgacag caccctccc actgacagac tctgtctgag 800
 aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacattctg 850
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 tgggagaag agaggcccg gaccccaga cccactgac ctacgctcc: 950
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 actgtcaaga tctctctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
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 tggccctct gccctgcac ctatgcact gtgaggatgg ccgcccagac 1150
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 agtggctgg aagtctgca agatttgcac agaggacaaa ccagacccctg 1250
 gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
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 aagaactcca gaaagaggca cagcacttc gaactctgc tggcccccac 1550
 gaaggctact ggaagctctt cctagcccag accttgagc tgaaggctac 1600
 ggcacgtcca gacaaagtga ccaagacata acaaaagcct aacagttcca 1650
 gatctgagct gtataattgt tcttattata tattaataaa taagaacttg 1700
 cattaccttc aaaaaaaaaa aaaaaaaaaa aa 1732

<110> 142
 <211> 451
 <112> FRT
 <113> Hum sapiens
 <400> 142

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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	
									25					30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	
									40					45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	
									55					60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	
									70					75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	
									85					90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	
									100					105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	
									115					120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	
									130					135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	
									145					150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	
									165					170	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	
									175					180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	
									190					195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	
									205					210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Ile	
									220					225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	
									235					240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	
									250					255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	
									265					270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	
									280					285	
Arg	Gln	Asp	Lys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Lys	

297	298	300
Arg His Pro Glu	Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro	
305	310	315
Gln Asp Lys Ala	Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg	
320	325	330
Cys Pro Lys Ala	Pro Gly Arg Val Leu Val His Thr Ser Val Ser	
335	340	345
Pro Ser Pro Asp	Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala	
350	355	360
Ser Asp Leu Val	Gln Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu	
365	370	375
Glu Thr Glu Ala	Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His	
380	385	390
Ser Gln Asn Leu	Pro Leu Asp Ser Asp Gln Gln Ser Gln Glu Ala	
395	400	405
Arg Leu Pro Glu	Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro	
410	415	420
Pro Arg Arg Ser	Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala	
425	430	435
Glu Gly His Gly	Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys	
440	445	450

Thr

<110> 143
 <111> 693
 <112> DNA
 <113> Homo sapiens

<400> 143
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 cttgggaaa atgtgatct cagtgcgaat gctggggcga ggggtggcg 150
 tgggtaacgc gctcctgtt atgtgaccc cgggagagcg ggggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaagganca gggaggagcc 250
 ggcaggaacc cagcagctat tctgggccc actgcaggag gaagcagca 300
 cggaggagaa cgtgggttgg aggaagaact ggatggttga cgtgagagc 350
 ggcagacac agagtcacc atgagacag acttcccttc ggggagcag 400
 caattgggt tggagcaat atcagaggc agcattctc cttggtggg 450

4010 144
 4011 93
 4012 FET
 4013 Homo sapiens

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<.10> 145
<.11> 1883
<.12> DNA
<.13> Homo sapiens
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22

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Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met
20 30

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35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu
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Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro
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Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys
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Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg
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Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr
200 205 210

Gly Glu Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro
215 220 225 230

Pro Gly Arg Pro Gly Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
230 235 240

Leu Ile Arg Ile Ala Leu Ala Asn Arg Thr Val Val Asp Ser Ser
241 250 259

270 Ile Thr Ala His Gly Ser Ile Thr Phe Tyr Gly Leu Thr Ala
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 280 Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala
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 290 Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys
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 300 Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro
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 310 Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr
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 320 Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile
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 330 Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala
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 340 Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu
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 350 Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly
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 395
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 catgccgtga ggtccattca cagaacacat ccctggctct catgctcagt 200
 ttgggttctga ctctctctaa gctgggatac aggcagtgga aggtgtttgg 250
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 attctctctt agagcaagc ctctctctga gctctctt cttactgtg 500

—

| | | |
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| 241 | 242 | 243 |
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| 249 | 250 | 251 |
| Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys | | |
| 252 | 253 | 254 |
| His Ala Val Glu Val Thr Leu Asp Pro Gln Thr Ala His Pro Lys | | |
| 259 | 260 | 261 |
| Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro | | |
| 262 | 263 | 264 |
| Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val | | |
| 269 | 270 | 271 |
| Val Ala Ser Gln Ser Phe Gln Ala Gly Lys His Tyr Trp Glu Val | | |
| 272 | 273 | 274 |
| Asp Gly Gly His Asn Lys Arg Trp Arg Val Gly Val Cys Arg Asp | | |
| 279 | 280 | 281 |
| Asp Val Asp Arg Arg Lys Glu Tyr Val Thr Leu Ser Pro Asp His | | |
| 282 | 283 | 284 |
| Gly Tyr Trp Val Leu Arg Leu Asn Gly Glu His Leu Tyr Phe Thr | | |
| 289 | 290 | 291 |
| Leu Asn Pro Arg Phe Ile Ser Val Phe Pro Arg Thr Pro Pro Thr | | |
| 292 | 293 | 294 |
| Lys Ile Gly Val Phe Leu Asp Tyr Glu Cys Gly Thr Ile Ser Phe | | |
| 299 | 300 | 301 |
| Phe Asn Ile Asn Asp Gln Ser Leu Ile Tyr Thr Leu Thr Cys Arg | | |
| 302 | 303 | 304 |
| Phe Glu Gly Leu Leu Arg Pro Tyr Ile Glu Tyr Pro Ser Tyr Asn | | |
| 309 | 310 | 311 |
| Glu Gln Asn Gly Thr Pro Ile Val Ile Cys Pro Val Thr Gln Glu | | |
| 312 | 313 | 314 |
| Ser Glu Lys Glu Ala Ser Trp Gln Arg Ala Ser Ala Ile Pro Glu | | |
| 319 | 320 | 321 |
| Thr Ser Asn Ser Glu Ser Ser Ser Gln Ala Thr Thr Pro Phe Leu | | |
| 322 | 323 | 324 |
| Pro Arg Gly Glu Met | | |
| 329 | | |

211-143

211-144

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Artificial

Artificial Sequence
1-24
Synthetic construct.

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150
11 23
DNA
Artificial

Artificial Sequence
1-23
Synthetic construct.

150
gagctgacc cagtgcctgac acc 23

151
11 45
DNA
Artificial

Artificial Sequence
1-45
Synthetic construct.

151
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152
11 94
DNA
Homo sapiens

152
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ggfeggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
atgdaatgac gtagcggagc cggcaatgag cagcctacac agcctggagc 150
gctcgccctt gtttgtctgc gtagcggagg ccgcggcagt cgcctcagcc 200
gctcggggg ggaatgtcac cagtgggggc ggggroggag ghaadgttga 250
cctatggagc ggcgcggggt tgggggggga ggcagacac ccttctctta 300
cttccaggc tcccaagac caggccaggc ggaaggggc ctccagcctc 350
cctatgacg gacatgacg tggacttc ctccagcctc ctccagcctc 400

| | | |
|-------------------------------------|-------------------------|---------------------|
| 170 | 175 | 180 |
| Ala Thr Glu Ala Pro Ser Ser Pr | Pr | Glu Tyr Val Cys Asn |
| 185 | 190 | 195 |
| Cys Ser Val Val Gly Ser Leu Asn Val | Asn Arg Cys Asn Gln Thr | |
| 200 | 205 | 210 |
| Thr Gly Gln Cys Glu Cys Arg Pro Gly | Tyr Gln Gly Leu His Cys | |
| 215 | 220 | 225 |
| Glu Thr Cys Lys Glu Gly Phe Tyr Leu | Asn Tyr Thr Ser Gly Leu | |
| 230 | 235 | 240 |
| Cys Gln Pro Cys Asp Cys Ser Pro His | Gly Ala Leu Ser Ile Pro | |
| 245 | 250 | 255 |
| Cys Asn Arg | | |

4210-154
 4211-14
 4212 DNA
 4213 Artificial

4220
 4221 Artificial Sequence
 4222 1-24
 4223 Synthetic construct.

4300-154
 4301 tctgctctg tggttggaag cctg 24

4310-155
 4311-24
 4312 DNA
 4313 Artificial

4400
 4401 Artificial Sequence
 4402 1-24
 4403 Synthetic construct.

4400-155
 4401 ccttcacatg gctgacagac ccac 24

4510-156
 4511-38
 4512 DNA
 4513 Artificial

4600
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 4602 1-38
 4603 Synthetic construct.

4600-156
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 ctggaacctg agcagcttct tgggacctgg taegtgttg cggtaggcctc 150
 ccgggaaaag ggttttgcca tggagaagga catgaagaac gtctgggggg 200
 tgggtgtgac cctcactcca gaaaacaacc tgggjaagct gtctctcag 250
 caagggtggg gagggtgtga ccagagtgtc atggacctga taaagcgaaa 300
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 tggtaggcac caacttcaga gactatgcca tctctttcac tcagctggag 400
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 <111> 163
 <112> PRT
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 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asn | Ser | Gly | Trp | Val | Phe | Glu | Asn | Pro | Ser | Ile | Gly | Val | Leu |
| | | | 105 | | | | | | 110 | | | | | 105 |
| Gln | Leu | Trp | Val | Leu | Ala | Thr | Asn | Phe | Arg | Asp | Tyr | Ala | Ile | Ile |
| | | | 110 | | | | | | 115 | | | | | 120 |
| Phe | Thr | Gln | Leu | Gln | Phe | Gly | Asp | Glu | Pro | Phe | Asn | Thr | Val | Glu |
| | | | 125 | | | | | | 130 | | | | | 135 |
| Leu | Tyr | Ser | Leu | Thr | Glu | Thr | Ala | Ser | Gln | Glu | Ala | Met | Gly | Leu |
| | | | 140 | | | | | | 145 | | | | | 150 |
| Ile | Thr | Lys | Trp | Ser | Arg | Ser | Leu | Gly | Phe | Leu | Ser | Gln | | |
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<213> Homo sapiens

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gtaaatgct gacgatgag agttccgtga cgggtccagga aggcctgtgt 150
gtccatgtgc cctgctcttt cctcaccac tcccatggct caatttacc 200
tgcccacgta gttcatggct actgggtccg ggaaggggcc aatacaaac 250
aggatgctcc agtggccaca aacaaccacg ctggggcagt gtgggaggag 300
actggggacc gattccacct ccttggggac ccacatacca agaattgcac 350
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| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Lys | Gly | Ser | Ile | Lys | Trp | Asn | Tyr | Lys | His | His | Arg | Leu | 110 | 111 | 112 |
| | | | | 125 | | | | | 130 | | | | | 135 | | | |
| Ser | Val | Asn | Val | Thr | Ala | Leu | Thr | His | Arg | Pro | Asn | Ile | Leu | Ile | 140 | 145 | 150 |
| Trp | Gly | Thr | Leu | Glu | Ser | Gly | Cys | Pro | Gln | Asn | Leu | Thr | Cys | Ser | 155 | 160 | 165 |
| Val | Pro | Trp | Ala | Cys | Glu | Gln | Gly | Thr | Phe | Pro | Met | Ile | Ser | Trp | 170 | 175 | 180 |
| Ile | Gly | Thr | Ser | Val | Ser | Pro | Leu | Asp | Pro | Ser | Thr | Thr | Arg | Ser | 185 | 190 | 195 |
| Ser | Val | Leu | Thr | Leu | Ile | Pro | Gln | Pro | Gln | Asp | His | Gly | Thr | Ser | 200 | 205 | 210 |
| Leu | Thr | Cys | Gln | Val | Thr | Phe | Pro | Gly | Ala | Ser | Val | Thr | Thr | Asn | 215 | 220 | 225 |
| Lys | Thr | Val | His | Leu | Asn | Val | Ser | Tyr | Pro | Pro | Gln | Asn | Leu | Thr | 230 | 235 | 240 |
| Met | Thr | Val | Phe | Gln | Gly | Asp | Gly | Thr | Val | Ser | Thr | Val | Leu | Gly | 245 | 250 | 255 |
| Asn | Gly | Ser | Ser | Leu | Ser | Leu | Pro | Glu | Gly | Gln | Ser | Leu | Arg | Leu | 260 | 265 | 270 |
| Val | Cys | Ala | Val | Asp | Ala | Val | Asp | Ser | Asn | Pro | Pro | Ala | Arg | Leu | 275 | 280 | 285 |
| Ser | Leu | Ser | Trp | Arg | Gly | Leu | Thr | Leu | Cys | Pro | Ser | Gln | Pro | Ser | 290 | 295 | 300 |
| Asn | Pro | Gly | Val | Leu | Glu | Leu | Pro | Trp | Val | His | Leu | Arg | Asp | Ala | 305 | 310 | 315 |
| Ala | Glu | Phe | Thr | Cys | Arg | Ala | Gln | Asn | Pro | Leu | Gly | Ser | Gln | Gln | 320 | 325 | 330 |
| Val | Tyr | Leu | Asn | Val | Ser | Leu | Gln | Ser | Lys | Ala | Thr | Ser | Gly | Val | 335 | 340 | 345 |
| Thr | Gln | Gly | Val | Val | Gly | Gly | Ala | Gly | Ala | Thr | Ala | Leu | Val | Phe | 350 | 355 | 360 |
| Leu | Ser | Phe | Cys | Val | Ile | Phe | Val | Val | Val | Arg | Ser | Cys | Arg | Lys | 365 | 370 | 375 |
| Lys | Ser | Ala | Arg | Pro | Ala | Ala | Gly | Val | Gly | Asp | Thr | Gly | Ile | Gln | 380 | 385 | 390 |
| Arg | Ala | Asn | Ala | Val | Arg | Gly | Ser | Ala | Ser | Gln | Gly | Pro | Leu | Thr | 395 | 400 | 405 |

Trp Ala Glu Asp Ser Pro Leu Asp Gln Pro Pro Pro Ala
410 415 420

Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
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Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
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Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
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<212> EST
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<400> 162
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Leu Ser Phe Thr Leu Glu Glu Gln Asp Ile Thr Gly Thr Trp Tyr

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| 23 | 24 | 25 |
| Leu Lys Ala Met Val Val Asp Lys Asp Ile Pro Glu Asp Arg Arg | | |
| 35 | 40 | 45 |
| Ile Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly | | |
| 50 | 55 | 60 |
| Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile | | |
| 65 | 70 | 75 |
| Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr | | |
| 80 | 85 | 90 |
| Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro | | |
| 95 | 100 | 105 |
| Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly | | |
| 110 | 115 | 120 |
| Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr | | |
| 125 | 130 | 135 |
| Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys | | |
| 140 | 145 | 150 |
| Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser | | |
| 155 | 160 | 165 |
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<211> 22

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<400> 163

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<211> 26

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<222> 1-26

<223> Synthetic construct.

<400> 164

ggagatgaag acctgttcc tg 26

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411 21
412 DNA
413 Artificial

4205
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4220 1-21
4230 Synthetic construct.

430 165
4310 cgtctcagga aagtccttat c 21

4410 166
4411 25
4412 DNA
4413 Artificial

4510
4511 Artificial Sequence
4520 1-25
4530 Synthetic construct.

4600 166
4610 cgtatgtggtt cgggaacgca gcttc 25

4710 167
4711 50
4712 DNA
4713 Artificial

4820
4811 Artificial Sequence
4820 1-50
4830 Synthetic construct.

490 167
4910 cagggaacctg gtacgtgaag gccatggtgg tcgataagga ctttcggag 50

5010 168
5011 45
5012 DNA
5013 Artificial

5110
5111 Artificial Sequence
5120 1-45
5130 Synthetic construct.

5200 168
5210 ctctctctca ccttgaggga ggaggatata acagggacct ggtac 45

5310 169
5311 1704
5312 DNA
5313 Homo sapiens

5410 169

1. Lys Gly Ala Thr Arg Ile Ile Lys Gly Ile Gln Cys Lys Pro
 30
 2. Ser Glu Pro Thr Gln Ala Ala Leu Ile Glu Lys Thr Arg Leu
 40
 3. Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
 50
 4. Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
 60
 5. Leu Gln Lys Glu Gln Gly Cys Glu Gln Thr Arg Thr Ala Thr
 70
 6. Glu Ser Ile Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
 80
 7. Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val
 90
 8. Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys
 100
 9. Val Thr Ala Gly Phe Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr
 110
 10. Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn
 120
 11. Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly
 130
 12. Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly
 140
 13. Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn
 150
 14. Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
 160
 15. Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
 170
 16. Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
 180

210. 171

211. 25

212. DNA

213. Artificial

220.

221. Artificial Sequence

222. 1-28

223. Synthetic construct.

<111> 171
 ...tgggattta tggg...

 <112> 172
 <113> 24
 <114> DNA
 <115> Artificial

 <116>
 <117> Artificial Sequence
 <118> 1-24
 <119> Synthetic construct.

 <120> 172
 ...c aggcga tgaagattct gcag 24

 <121> 173
 <122> 18
 <123> DNA
 <124> Artificial

 <125>
 <126> Artificial Sequence
 <127> 1-18
 <128> Synthetic construct.

 <129> 173
 ...cttttgtct gtaaccag 18

 <130> 174
 <131> 24
 <132> DNA
 <133> Artificial

 <134>
 <135> Artificial Sequence
 <136> 1-24
 <137> Synthetic construct.

 <138> 174
 ...ctgtgatct tgcggygcta ggcg 24

 <139> 175
 <140> 25
 <141> DNA
 <142> Artificial

 <143>
 <144> Artificial Sequence
 <145> 1-25
 <146> Synthetic construct.

 <147> 175
 ...ctatctca ccaggatttc ggga 21

 <148> 176
 <149> 15
 <150> DNA

<100> Artificial

<101> Artificial Sequence
 <102> 1-18
 <103> Synthetic construct.

<400> 176
 ttaatga tctggtc 18

<100> 177
 <101> 50
 <102> DNA
 <103> Artificial

<100>
 <101> Artificial Sequence
 <102> 1-50
 <103> Synthetic construct.

<400> 177
 agccatgag gattctcag ttaatccctgc ttgctctggc aacagggctt 50

<100> 178
 <101> 43
 <102> DNA
 <103> Artificial

<100>
 <101> Artificial Sequence
 <102> 1-43
 <103> Synthetic construct.

<400> 178
 gagagaccag gatcatcaag gggttcgagt gcaagcctca etc 43

<100> 179
 <101> 207
 <102> DNA
 <103> Homo sapiens

<400> 179
 gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50
 gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100
 aagaaaagagg adagcaacga agaaagtgaaa atagaagttt tgcattgtcc 150
 aaaaattgc tctaagacaa gcaagaaggg agacctacta aatgccatt 200
 ataaagata cctggctaaa caacgctega aattctactg cagccggaca 250
 aaaaatgaag gacacccaa atgatttgtt cttgatgttg acaaatcat 300
 aaatctata gactttcta tgacatatat gtacctgga aaaaagaaa 350
 attattat gctcttca tttctatg aaaaagaag atgtgaaa 400

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 181 | Thr | Phe | Lys | Gln | Ile | Arg | Met | Asp | Asn | Asp | Arg | Gln | Leu |
| | | | 175 | | | | | 180 | | | | | 185 |
| 186 | Lys | Ala | Gln | Ile | Asn | Leu | Tyr | Leu | Gln | Arg | Glu | Phe | Gln |
| | | | 170 | | | | | 175 | | | | | 180 |
| 191 | Glu | Lys | Phe | Arg | Asp | Lys | Ser | Tyr | Gln | Asp | Ala | Val | Leu |
| | | | 185 | | | | | 190 | | | | | 195 |
| 201 | Ile | Phe | Lys | Lys | Asn | Asp | His | Asp | Gly | Asp | Gly | Phe | Ile |
| | | | 200 | | | | | 205 | | | | | 210 |
| 211 | Lys | Glu | Tyr | Asn | Val | Tyr | Gln | His | Asp | Glu | Leu | | |
| | | | 215 | | | | | 220 | | | | | |

<210> 181

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<230> 181

<231> attctctact ggagccgata cc 22

<232> 181

<233> 18

<234> DNA

<235> Artificial

<240>

<241> Artificial Sequence

<242> 1-18

<243> Synthetic construct.

<250> 182

<251> gacatggaca atgacagg 18

<260> 183

<261> 18

<262> DNA

<263> Artificial

<270>

<271> Artificial Sequence

<272> 1-18

<273> Synthetic construct.

<280> 183

<281> attttcaga tptatnd 18

<290> 184

<291> 16

<292> DNA

<293> Artificial

411 Artificial Sequence
412 1-18
413 Synthetic construct.

414-184
atctctgtcc acccccaaa 18

415-185
416 27
417 PNA
418 Artificial

419
420 Artificial Sequence
421 1-27
422 Synthetic construct.

423-185
atctctgat atgaattgtc acgtggc 27

424-186
425 24
426 DNA
427 Artificial

428
429 Artificial Sequence
430 1-24
431 Synthetic construct.

432-186
ctctagaggg aagaggaatt gcac 24

433-187
434 52
435 DNA
436 Artificial

437
438 Artificial Sequence
439 1-52
440 Synthetic construct.

441-187
accctatttg acggctacct gactaaagac ggcctgaaat tctactgcag 50
cc 12

442-188
443 573
444 PNA
445 Homo sapiens

446-188
ctgagatgta gaaacattg ctctcttctg cttctattt ttgtgtgaa 50
ctctctggaa ctgtcttctg gaaacattg cttctattt ctgaattg 100

atatttgcg atgtggttt atattttta cttttccctt atgttttt 150
 attttgcg atgtggttt atattttta cttttccctt atgttttt 200
 attttgcg atgtggttt atattttta cttttccctt atgttttt 250
 attttgcg atgtggttt atattttta cttttccctt atgttttt 300
 attttgcg atgtggttt atattttta cttttccctt atgttttt 350
 attttgcg atgtggttt atattttta cttttccctt atgttttt 400
 attttgcg atgtggttt atattttta cttttccctt atgttttt 450
 attttgcg atgtggttt atattttta cttttccctt atgttttt 500
 attttgcg atgtggttt atattttta cttttccctt atgttttt 550
 attttgcg atgtggttt atattttta cttttccctt atgttttt 600

(210) 189
 (211) 74
 (212) FRT
 (213) Homo sapiens

(200) 189
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
 1 5 10
 Ser Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
 20 25 30
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
 35 40 45
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
 50 55 60
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
 65 70

(210) 190
 (211) 24
 (212) DNA
 (213) Artificial

(200)
 (210) Artificial Sequence
 (211) 1-24
 (212) Synthetic construct

(200) 190
 atgttgcg atgttgcg atgttgcg atgttgcg atgttgcg 24

(210) 191
 (211) 24
 (212) DNA
 (213) Artificial

<400> 191
Artificial Sequence
1-14
Synthetic construct.

<400> 191
Attacutgt ctccaaagg cta 24

<400> 192
111 50
112 DNA
113 Artificial

<400>
111 Artificial Sequence
112 1-50
113 Synthetic construct.

<400> 192
ccgtgtgctaa gtgccccca aatgttctt gtgtcaataa cactcaatgc 50

<400> 193
111 1091
112 DNA
113 Homo sapiens

<400> 193
caagcaggtc atcccccttg taaccttcaa agacaagcag agaaagcaga 50
gggggggggc acagggaagg gttacctct gagattccc ttctcccaca 100
gactttggaa gtgaccacac atgagggtca gcatcttttt gctcctgtgt 150
gttcttggggc tcagccaggc agccacacgc aagattttca atggcaatga 200
gtgtgggggt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcttgcgctg cgggggtgtc ctattgacc acaggtgggt cctcacacgc 300
gctcaatgca ggggcagtag gtactgggtg cgcctggggg aacaaagcct 350
cagccagctc gactggacc agcagatccg gcacagggc ttctctgtga 400
cccatccggc ctacctggga gctcgacga gccacgacga cgaacctcgg 450
ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttaaccct 500
gacctgcgc aatgaactgt cagcggtg caccagtagc caggtctaa 550
gttggggcat caccacacac cagcgaacc cattcccga tetgtccag 600
tgcctcaac tetccatgt ctccatgac acctccata ctgtatcc 650
caggagaatc acgagctca tttctttac aaggagctc caggacaga 700
attctaca agtgaattc cagcagcag cgttttga ggaattct 750
cagcagga tgcctttaa atcttggg ccttttaa cctgaat 800

...
 ...
 ...
 ...
 ...
 ...
 ...

<10> 194
 <11> 248
 <12> PRT
 <13> Homo sapiens

<400> 194
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 1 5 10 15
 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
 20 25 30
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
 35 40 45
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
 50 55 60
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
 65 70 75
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
 80 85 90
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
 95 100 105
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
 110 115 120
 Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
 125 130 135
 Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
 140 145 150
 Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
 155 160 165
 Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
 170 175 180
 Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
 185 190 194

| | | |
|---|-----|-----|
| 20 | 100 | 120 |
| Gly Ile Val Ser Trp Gly Ser Val Gly Trp Tyr Gly Glu Asp | | |
| 215 | 220 | 225 |
| Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp | | |
| 230 | 235 | 240 |
| Asp Met Ile Met Arg Asn Asn | | |
| 245 | | |

<110> 195
 <111> 1485
 <112> DNA
 <113> Homo sapiens

<400> 195
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 ctgtctcctc gccgcgtccg cgaagccttg agccacggg agcccccgcg 100
 tggcatgtc ggcgcagctc agcaacaggt tccacggagg gaagggcttc 150
 ggcttgctca aagccccgca ggagaggagg ctggccgaga tcaacccgga 200
 gttttctgtg gccacagaat acagtgtatg agagacctt ccagaaagc 250
 tccagcctt caaagadaag tacatggagt ttgacctaa caatgaagga 300
 gagattgac agatgtctt cagaggatg atgagagc ttgtgtccc 350
 caagacccac ctgagatga agaagatgat ctcaagggtg acaggagggg 400
 ccagtgcac tatatcctac agagactttg tgaacatgat gctggggaaa 450
 cggctgggctg tctcaagtt agtcatgag ttggaaggaa aagccaaaga 500
 gaggagccc aagccayttg gcccccctcc acagacagac attgtatagc 550
 tgcctgagg acccgcctg gactcccag cctcccacc ccatacctcc 600
 ctcccgatct tctgcctct ttgacacac tgtgatctct ctctctctca 650
 ttgttttgt catlgagggt ttgttttgt ttccatcaat gtctttgtaa 700
 agcacaatt atctgcctta aaggggtct cugtcggga atctgagcc 750
 ttgggtccc tccctctct cttccctct tcccctcc ctatgagaa 800
 ggtctgatat caaacacaa atagagggg gtaggcag agcagaggg 850
 ctccagcct gtatctctt cacttgagg aacacagct ctccatctt 900
 tccagagtg tccacacaa attcaggtc actcaatca ctctgagag 950
 acacaggg caatctaa acactttaa gtaggaa actcagga 1000
 cctctctt cctctctt cctctctt cctctctt cctctctt 1050

197

gagagatcc gagatcc gagatcc gagatcc gagatcc 50
gagatcc gagatcc gagatcc gagatcc gagatcc 100
gagatcc gagatcc gagatcc gagatcc gagatcc 150
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gagatcc gagatcc gagatcc gagatcc gagatcc 1450

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 tttatgtttatgttccattc tctggttca tttatgtttatgttccattc 385
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 aacattgcca cctgctgtga cggattcagc aattcattgt ctattcattc 395
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 ctgagctgaa cctctgtcag cactgagcagc agtcattcag cctcagcagc 405
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 aaacaaaaaa tagaactcaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198
 <211> 1523
 <212> PFT
 <213> Homo sapiens

<400> 198
 Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg
 1 5 10 15
 Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro
 20 25 30
 Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val
 35 40 45
 Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
 50 55 60
 Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
 65 70 75
 Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
 80 85 90
 His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
 95 100 105
 Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
 110 115 120
 Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
 125 130 135
 Thr Arg Leu Asp Leu Ser Gln Asn Gln Ile Gln Gly Ile Pro Arg
 140 145 150
 Lys Ala Phe Arg Gly Ile Thr Arg Val Lys Asn Leu Gln Leu Asp
 155 160 165

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Asn | His | Ile | Ser | Cys | Ile | Glu | Asp | Gly | Ala | His | Arg | Ala | Leu | |
| | | | | 170 | | | | | 171 | | | | | 172 | |
| Arg | Asp | Leu | Glu | Ile | Leu | Thr | Leu | Asn | Asn | Asn | Asn | Ile | Ser | Arg | |
| | | | | 181 | | | | | 182 | | | | | 183 | |
| Ile | Leu | Val | Thr | Ser | Phe | Asn | His | Met | Pro | Lys | Ile | Arg | Thr | Leu | |
| | | | | 190 | | | | | 191 | | | | | 192 | |
| Arg | Leu | His | Ser | Asn | His | Leu | Tyr | Cys | Asp | Cys | His | Leu | Ala | Trp | |
| | | | | 205 | | | | | 206 | | | | | 207 | |
| Leu | Ser | Asp | Trp | Leu | Arg | Gln | Arg | Arg | Thr | Val | Gly | Gln | Phe | Thr | |
| | | | | 210 | | | | | 211 | | | | | 212 | |
| Leu | Cys | Met | Ala | Pro | Val | His | Leu | Arg | Gly | Phe | Asn | Val | Ala | Asp | |
| | | | | 215 | | | | | 216 | | | | | 217 | |
| Val | Gln | Lys | Lys | Glu | Tyr | Val | Cys | Pro | Ala | Pro | His | Ser | Glu | Pro | |
| | | | | 260 | | | | | 261 | | | | | 262 | |
| Pro | Ser | Cys | Asn | Ala | Asn | Ser | Ile | Ser | Cys | Pro | Ser | Pro | Cys | Thr | |
| | | | | 275 | | | | | 276 | | | | | 277 | |
| Cys | Ser | Asn | Asn | Ile | Val | Asp | Cys | Arg | Gly | Lys | Gly | Leu | Met | Glu | |
| | | | | 280 | | | | | 281 | | | | | 282 | |
| Ile | Pro | Ala | Asn | Leu | Pro | Glu | Gly | Ile | Val | Glu | Ile | Arg | Leu | Gln | |
| | | | | 305 | | | | | 306 | | | | | 307 | |
| Gln | Asn | Ser | Ile | Lys | Ala | Ile | Pro | Ala | Gly | Ala | Phe | Thr | Gln | Tyr | |
| | | | | 310 | | | | | 311 | | | | | 312 | |
| Lys | Lys | Leu | Lys | Arg | Ile | Asp | Ile | Ser | Lys | Asn | Gln | Ile | Ser | Asp | |
| | | | | 335 | | | | | 336 | | | | | 337 | |
| Ile | Ala | Pro | Asp | Ala | Phe | Gln | Gly | Leu | Lys | Ser | Leu | Thr | Ser | Leu | |
| | | | | 350 | | | | | 351 | | | | | 352 | |
| Val | Leu | Tyr | Gly | Asn | Lys | Ile | Thr | Glu | Ile | Ala | Lys | Gly | Leu | Phe | |
| | | | | 365 | | | | | 366 | | | | | 367 | |
| Asp | Gly | Leu | Val | Ser | Leu | Gln | Leu | Leu | Leu | Leu | Asn | Ala | Asn | Lys | |
| | | | | 380 | | | | | 381 | | | | | 382 | |
| Ile | Asn | Cys | Leu | Arg | Val | Asn | Thr | Phe | Gln | Asp | Leu | Gln | Asn | Leu | |
| | | | | 395 | | | | | 396 | | | | | 397 | |
| Asn | Leu | Leu | Ser | Leu | Tyr | Asp | Asn | Lys | Leu | Gln | Thr | Ile | Ser | Lys | |
| | | | | 410 | | | | | 411 | | | | | 412 | |
| Gly | Leu | Phe | Ala | Pro | Leu | Gln | Ser | Ile | Gln | Thr | Leu | His | Leu | Ala | |
| | | | | 425 | | | | | 426 | | | | | 427 | |
| Gln | Asn | Pro | Phe | Val | Cys | Asp | Cys | His | Leu | Lys | Trp | Leu | Ala | Asp | |
| | | | | 440 | | | | | 441 | | | | | 442 | |
| Tyr | Leu | Phe | Asp | Asn | Pro | Ile | Gln | Thr | Ser | Gly | Ala | Arg | Cys | Ser | |

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|-----------------|---|-------------------------|-----|--|-----|
| | 455 | | 460 | | 465 |
| Leu Ile Arg Arg | Leu Ala Asn Lys Arg | Ile Ser Gln Ile Lys Ser | | | |
| | 470 | | 475 | | 480 |
| Lys Lys Phe Arg | Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe | | | | |
| | 485 | | 490 | | 495 |
| Ile Ser Glu Cys | Phe Met Asp Leu Val | Cys Pro Glu Lys Cys Arg | | | |
| | 500 | | 505 | | 510 |
| Cys Glu Gly Thr | Ile Val Asp Cys Ser | Asn Gln Lys Leu Val Arg | | | |
| | 515 | | 520 | | 525 |
| Ile Pro Ser His | Leu Pro Glu Tyr Val | Thr Asp Leu Arg Leu Asn | | | |
| | 530 | | 535 | | 540 |
| Asp Asn Glu Val | Ser Val Leu Glu Ala | Thr Gly Ile Phe Lys Lys | | | |
| | 545 | | 550 | | 555 |
| Leu Pro Asn Leu | Arg Lys Ile Asn Leu | Ser Asn Asn Lys Ile Lys | | | |
| | 560 | | 565 | | 570 |
| Glu Val Arg Glu | Gly Ala Phe Asp Gly | Ala Ala Ser Val Gln Glu | | | |
| | 575 | | 580 | | 585 |
| Leu Met Leu Thr | Gly Asn Gln Leu Glu | Thr Val His Gly Arg Val | | | |
| | 590 | | 595 | | 600 |
| Phe Arg Gly Leu | Ser Gly Leu Lys Thr | Leu Met Leu Arg Ser Asn | | | |
| | 605 | | 610 | | 615 |
| Leu Ile Ser Cys | Val Ser Asn Asp Thr | Phe Ala Gly Leu Ser Ser | | | |
| | 620 | | 625 | | 630 |
| Val Arg Leu Leu | Ser Leu Tyr Asp Asn Arg | Ile Thr Thr Ile Thr | | | |
| | 635 | | 640 | | 645 |
| Pro Gly Ala Phe | Thr Thr Leu Val Ser | Leu Ser Thr Ile Asn Leu | | | |
| | 650 | | 655 | | 660 |
| Leu Ser Asn Pro | Phe Asn Cys Asn Cys | His Leu Ala Trp Leu Gly | | | |
| | 665 | | 670 | | 675 |
| Lys Trp Leu Arg | Lys Arg Arg Ile Val | Ser Gly Asn Pro Arg Cys | | | |
| | 680 | | 685 | | 690 |
| Gln Lys Pro Phe | Phe Leu Lys Glu Ile | Pro Ile Gln Asp Val Ala | | | |
| | 695 | | 700 | | 705 |
| Ile Gln Asp Phe | Thr Cys Asp Gly Asn | Glu Glu Ser Ser Cys Gln | | | |
| | 710 | | 715 | | 720 |
| Leu Ser Pro Arg | Cys Pro Glu Gln Cys | Thr Cys Met Glu Thr Val | | | |
| | 725 | | 730 | | 735 |
| Val Arg Lys Ser | Asn Lys Gly Leu Arg | Ala Leu Trp Arg Gly Met | | | |
| | 740 | | 745 | | 750 |

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|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 774 | Arg | Val | Thr | Gln | Leu | Tyr | Leu | Glu | Gly | Asn | His | Leu | Thr | 775 |
| 777 | Arg | Val | Pro | Arg | Gln | Leu | Ser | Ala | Leu | Arg | His | Leu | Thr | 780 |
| 780 | Arg | Leu | Ser | Asn | Asn | Ser | Ile | Ser | Met | Leu | Thr | Asn | Tyr | 795 |
| 806 | Ser | Asn | Met | Ser | His | Leu | Ser | Thr | Leu | Ile | Leu | Ser | Tyr | 810 |
| 815 | Leu | Arg | Cys | Ile | Pro | Val | His | Ala | Phe | Asn | Gly | Leu | Arg | 825 |
| 830 | Arg | Val | Leu | Thr | Leu | His | Gly | Asn | Asp | Ile | Ser | Ser | Val | 840 |
| 845 | Gly | Ser | Phe | Asn | Asp | Leu | Thr | Ser | Leu | Ser | His | Leu | Ala | 855 |
| 860 | Thr | Asn | Pro | Leu | His | Cys | Asp | Cys | Ser | Leu | Arg | Trp | Leu | 870 |
| 875 | Trp | Val | Lys | Ala | Gly | Tyr | Lys | Glu | Pro | Gly | Ile | Ala | Arg | 885 |
| 890 | Ser | Pro | Glu | Pro | Met | Ala | Asp | Arg | Leu | Leu | Leu | Thr | Thr | 900 |
| 905 | His | Arg | Phe | Gln | Cys | Lys | Gly | Pro | Val | Asp | Ile | Asn | Ile | 915 |
| 920 | Lys | Cys | Asn | Ala | Cys | Leu | Ser | Ser | Pro | Cys | Lys | Asn | Asn | 930 |
| 935 | Cys | Thr | Gln | Asp | Pro | Val | Glu | Leu | Tyr | Arg | Cys | Ala | Cys | 945 |
| 950 | Ser | Tyr | Lys | Gly | Lys | Asp | Cys | Thr | Val | Pro | Ile | Asn | Thr | 960 |
| 965 | Gln | Asn | Pro | Cys | Gln | His | Gly | Gly | Thr | Cys | His | Leu | Ser | 975 |
| 980 | His | Lys | Asp | Gly | Phe | Ser | Cys | Ser | Cys | Pro | Leu | Gly | Phe | 990 |
| 995 | Gln | Arg | Cys | Glu | Ile | Asn | Pro | Asp | Asp | Cys | Glu | Asp | Asn | 1005 |
| 1010 | Glu | Asn | Asn | Ala | Thr | Cys | Val | Asp | Gly | Ile | Asn | Asn | Tyr | 1020 |
| 1025 | Ile | Cys | Pro | Pro | Asn | Tyr | Thr | Gly | Glu | Leu | Cys | Arg | Gln | 1035 |
| | Arg | His | Cys | Val | Pro | Gln | Leu | Asn | Leu | Cys | Gln | His | Gln | |

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| 104 | 1045 | 1049 |
| Leu Asp Lys Gly Phe Ser Cys Gln Cys Val Pro Gly | | |
| 1055 | 1060 | 1065 |
| Tyr Ser Gly Lys Leu Cys Gln Thr Asp Asn Asp Asp Cys Val Ala | | |
| 1070 | 1075 | 1080 |
| Leu Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly | | |
| 1085 | 1090 | 1095 |
| Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Gln | | |
| 1100 | 1105 | 1110 |
| His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln | | |
| 1115 | 1120 | 1125 |
| Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Gln | | |
| 1130 | 1135 | 1140 |
| Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Gln | | |
| 1145 | 1150 | 1155 |
| Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Gln | | |
| 1160 | 1165 | 1170 |
| Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln | | |
| 1175 | 1180 | 1185 |
| Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp | | |
| 1190 | 1195 | 1200 |
| Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu | | |
| 1205 | 1210 | 1215 |
| Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val | | |
| 1220 | 1225 | 1230 |
| Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr | | |
| 1235 | 1240 | 1245 |
| Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys | | |
| 1250 | 1255 | 1260 |
| Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser | | |
| 1265 | 1270 | 1275 |
| Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala | | |
| 1280 | 1285 | 1290 |
| Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys | | |
| 1295 | 1300 | 1305 |
| Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala | | |
| 1310 | 1315 | 1320 |
| Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys | | |
| 1325 | 1330 | 1335 |

Thr Val Cys Lys His Gly Leu Tyr Arg Ser Val Glu Lys Asp Ser
1345 1345 1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
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Glu Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
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Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
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Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
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Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
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Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
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Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
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Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
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Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
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Glu Cys Gly Cys Leu Ala Cys Ser
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<400> 199

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<114> 200

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<413> Homo sapiens

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cgggcattct gacctcatt ggttgccctg tccaggcgcc cgagtccaaa 200
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gactatggca tcttccagat caacagcttc gcttggtgca gacggggaaa 400
gctgaaggag aacaaccact gccatgtccc ctgctcagcc ttgatcaactg 450
atgacctcac agatgcattt atctgtgcca ggaaaattgt taaagagaca 500
caaggaatga actattggca aggettggaag aaacattgtg agggcagaga 550
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gttttttt

<110> 143
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 <112> 145
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<110> 203

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| 1 | | | | 5 | | | | | 10 | | | | | 15 |
| Gly | Ala | Glu | Ser | Lys | Ile | Tyr | Thr | Arg | Cys | Lys | Leu | Ala | Lys | Ile |
| | | | | 20 | | | | | 25 | | | | | 30 |
| Phe | Ser | Arg | Ala | Gly | Leu | Asp | Asn | Tyr | Trp | Gly | Phe | Ser | Leu | Gly |
| | | | | 35 | | | | | 40 | | | | | 45 |
| Asn | Trp | Ile | Cys | Met | Ala | Tyr | Tyr | Glu | Ser | Gly | Tyr | Asn | Thr | Thr |
| | | | | 50 | | | | | 55 | | | | | 60 |
| Ala | Pro | Thr | Val | Leu | Asp | Asp | Gly | Ser | Ile | Asp | Tyr | Gly | Ile | Phe |
| | | | | 65 | | | | | 70 | | | | | 75 |
| Gln | Ile | Asn | Ser | Phe | Ala | Trp | Cys | Arg | Arg | Gly | Lys | Leu | Lys | Glu |
| | | | | 80 | | | | | 85 | | | | | 90 |
| Asn | Asn | His | Cys | His | Val | Ala | Cys | Ser | Ala | Leu | Ile | Thr | Asp | Asp |
| | | | | 95 | | | | | 100 | | | | | 105 |
| Leu | Thr | Asp | Ala | Ile | Ile | Cys | Ala | Arg | Lys | Ile | Val | Lys | Glu | Thr |
| | | | | 110 | | | | | 115 | | | | | 120 |
| Gln | Gly | Met | Asn | Tyr | Trp | Gln | Gly | Trp | Lys | Lys | His | Cys | Glu | Gly |
| | | | | 125 | | | | | 130 | | | | | 135 |
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acagagctttg aggtatgaagg ctac 24

<110> 205
 <111> 24
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<110>

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Artificial Sequence
1-24
Synthetic construct.

400 306
cctctggcac aggtctctcc cctc 24

410 307
411 24
412 DNA
413 Artificial

420
421 Artificial Sequence
422 1-24
423 Synthetic construct.

430 307
tctcttaccg aggcctagca ggcg 24

440 308
441 47
442 DNA
443 Artificial

450
451 Artificial Sequence
452 1-47
453 Synthetic construct.

460 308
ctacacctcg tgcacactgg caaaaatatt ctcgagggct ggcttg 47

470 309
471 1648
472 DNA
473 Homo sapiens

480 309
caggccattt gcatccact gtccttgtgt tcggagccag gccacaccgt 50
ctcaggaact gtcagtgttt aaaaaagcca agctgaatat atcatgcccc 100
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Experiments

| | | | | | | | | | | | | |
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| 1 | Leu | Lys | Leu | Val | His | Gly | Ser | Phe | Leu | Val | Phe | Gly |
| | | | | | | | 10 | | | | | 15 |
| 2 | Lys | Phe | Lys | Leu | Phe | Thr | Leu | Val | Ser | Ala | Cys | Ile |
| | | | 20 | | | | | | 35 | | | 30 |
| 3 | Leu | Ala | Arg | Arg | Arg | Lys | Lys | Ile | Leu | Phe | Tyr | Cys |
| | | | 35 | | | | | 40 | | | | 45 |
| 4 | Asp | Leu | Leu | Leu | Thr | Lys | Arg | Asp | Ser | Phe | Leu | Lys |
| | | | 50 | | | | | 55 | | | | 60 |
| 5 | Arg | Ala | Pro | Ile | Asp | Trp | Ile | Glu | Glu | Tyr | Thr | Thr |
| | | | 65 | | | | | 70 | | | | 75 |
| 6 | Ala | Asp | Cys | Ile | Leu | Val | Asn | Ser | Glu | Phe | Thr | Ala |
| | | | 80 | | | | | | 85 | | | 90 |
| 7 | Lys | Glu | Thr | Phe | Lys | Ser | Leu | Ser | His | Ile | Asp | Pro |
| | | | 95 | | | | | | 100 | | | 105 |
| 8 | Tyr | Pro | Ser | Leu | Asn | Val | Thr | Ser | Phe | Asp | Ser | Val |
| | | | 110 | | | | | | 115 | | | 120 |
| 9 | Lys | Leu | Asp | Asp | Leu | Val | Pro | Lys | Gly | Lys | Lys | Phe |
| | | | 125 | | | | | | 130 | | | 135 |
| 10 | Ser | Ile | Asn | Arg | Tyr | Glu | Arg | Lys | Lys | Asn | Leu | Thr |
| | | | 140 | | | | | | 145 | | | 150 |
| 11 | Glu | Ala | Leu | Val | Gln | Leu | Arg | Gly | Arg | Leu | Thr | Ser |
| | | | 155 | | | | | | 160 | | | 165 |
| 12 | Glu | Arg | Val | His | Leu | Ile | Val | Ala | Gly | Gly | Tyr | Asp |
| | | | 170 | | | | | | 175 | | | 180 |
| 13 | Leu | Glu | Asn | Val | Glu | His | Tyr | Gln | Glu | Leu | Lys | Lys |
| | | | 185 | | | | | | 190 | | | 195 |
| 14 | Gln | Gln | Ser | Asp | Leu | Gly | Gln | Tyr | Val | Thr | Phe | Leu |
| | | | 200 | | | | | | 205 | | | 210 |
| 15 | Asp | Lys | Gln | Lys | Ile | Ser | Leu | Leu | His | Ser | Cys | Thr |
| | | | 215 | | | | | | 220 | | | 225 |
| 16 | Tyr | Thr | Pro | Ser | Asn | Glu | His | Phe | Gly | Ile | Val | Pro |
| | | | 230 | | | | | | 235 | | | 240 |
| 17 | Met | Tyr | Met | Gln | Cys | Pro | Val | Ile | Ala | Val | Asn | Ser |
| | | | 245 | | | | | | 250 | | | 255 |
| 18 | Glu | Ser | Ile | Asp | His | Ser | Val | Thr | Gly | Phe | Leu | Cys |
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 Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
 50 55 60
 Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
 65 70 75
 Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
 80 85 90
 Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
 95 100 105
 Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
 110 115 120
 His Met Arg Lys Lys Leu Tyr Gln Asn Gly Val Thr Asp Ser Leu
 125 130 135
 Lys Ser Asn Phe Ala Ile Leu Leu Lys Leu Ser Glu Glu Leu Leu

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| 147 | 148 | 149 |
| Asp Lys Trp Leu Ser Tyr Phe Gln Thr Gln His Val Trp Leu Ser | | |
| 155 | 167 | 168 |
| Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val | | |
| 170 | 175 | 180 |
| Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln | | |
| 185 | 190 | 195 |
| Lys Asn His Gly Thr Val Trp Ser Gln Ile Gly Lys Gly Phe Leu | | |
| 200 | 205 | 210 |
| Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Gln | | |
| 215 | 220 | 225 |
| Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys | | |
| 230 | 235 | 240 |
| Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser | | |
| 245 | 250 | 255 |
| Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser | | |
| 260 | 265 | 270 |
| Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys | | |
| 275 | 280 | 285 |
| Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Gln Gln Val Gln Lys | | |
| 290 | 295 | 300 |
| Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val | | |
| 305 | 310 | 315 |
| Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu | | |
| 320 | 325 | 330 |
| Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln | | |
| 335 | 340 | 345 |
| Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg | | |
| 350 | 355 | 360 |
| Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro | | |
| 365 | 370 | 375 |
| Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp | | |
| 380 | 385 | 390 |
| Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly | | |
| 395 | 400 | 405 |
| Thr Gln Glu Cys Pro Gln Leu Arg Phe Ala Tyr Met Val Thr Thr | | |
| 410 | 415 | 420 |
| Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val | | |
| 425 | 430 | 435 |

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 110 Gly Leu Phe Ala Val Thr Leu Ala Gly Phe Leu Ser Gly Val
 120 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
 130 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
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1.1.1.16

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20 25
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
35 40
Ala Gln His Leu Ser Leu Ile Leu Arg Tyr Val Val Val Ser
50 55
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
65 70
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
80 85
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
95 100
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
110 115
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
125 130
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
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Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
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Pro

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 Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
 65 70 75
 Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
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 Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
 95 100 105
 Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
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 Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
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 Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
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Ser Cys Ser Thr Pro Phe Lys Val Val Cys Val Tyr Thr Ala His
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 ttcaaatatc ccatattcaa atttagtgca atatcttgtc ttttgtatag 2000
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 Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Ile | Ser | Val | Arg | Ala | Ala | Asn | Ser | Lys | Val | Ala | Phe | Ser | Ala | |
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| Val | Arg | Ser | Thr | Asn | His | Glu | Pro | Ser | Glu | Met | Ser | Asn | Lys | Thr | |
| | | | | 80 | | | | | 85 | | | | | 90 | |
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| Phe | Thr | Leu | Glu | Ser | Val | Phe | Val | Ala | Pro | Arg | Lys | Gly | Ile | Tyr | |
| | | | | 110 | | | | | 115 | | | | | 120 | |
| Ser | Phe | Ser | Phe | His | Val | Ile | Lys | Val | Tyr | Gln | Ser | Gln | Thr | Ile | |
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| Gln | Val | Asn | Leu | Met | Leu | Asn | Gly | Lys | Pro | Val | Ile | Ser | Ala | Phe | |
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| Ala | Gly | Asp | Lys | Asp | Val | Thr | Arg | Glu | Ala | Ala | Thr | Asn | Gly | Val | |
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| Leu | Leu | Tyr | Leu | Asp | Lys | Glu | Asp | Lys | Val | Tyr | Leu | Lys | Leu | Glu | |
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| Lys | Gly | Asn | Leu | Val | Gly | Gly | Trp | Gln | Tyr | Ser | Thr | Phe | Ser | Gly | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Phe | Leu | Val | Phe | Pro | Leu | | | | | | | | | | |
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 c213> Artificial

c210>
 c211> Artificial Sequence
 c212> 1-20
 c213> Synthetic construct.

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c210> 222
 c211> 24
 c212> DNA
 c213> Artificial

c210>
 c211> Artificial Sequence
 c212> 1-24
 c213> Synthetic construct.

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c210> 221
 c211> 4

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<212> 187

411 - Homo sapiens

411 - 225

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| Met | Thr | Ala | Ala | Val | Phe | Phe | Gly | Cys | Ala | Phe | Ile | Ala | Phe | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Leu | Ala | Leu | Tyr | Val | Phe | Thr | Ile | Ala | Ile | Glu | Pro | Leu |
| | | | | 20 | | | | | 25 | | | | | 30 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Ile | Phe | Leu | Ile | Ala | Gly | Ala | Phe | Phe | Trp | Leu | Val | Ser |
| | | | | 35 | | | | | 40 | | | | | 45 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Ile | Ser | Ser | Leu | Val | Trp | Phe | Met | Ala | Arg | Val | Ile | Ile |
| | | | | 50 | | | | | 55 | | | | | 60 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Asn | Lys | Asp | Gly | Pro | Thr | Gln | Lys | Tyr | Leu | Leu | Ile | Phe | Gly |
| | | | | 65 | | | | | 70 | | | | | 75 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Phe | Val | Ser | Val | Tyr | Ile | Gln | Glu | Met | Phe | Arg | Phe | Ala | Tyr |
| | | | | 80 | | | | | 85 | | | | | 90 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Lys | Leu | Leu | Lys | Lys | Ala | Ser | Glu | Gly | Leu | Lys | Ser | Ile | Asn |
| | | | | 95 | | | | | 100 | | | | | 105 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Glu | Thr | Ala | Pro | Ser | Met | Arg | Leu | Leu | Ala | Tyr | Val | Ser |
| | | | | 110 | | | | | 115 | | | | | 120 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | Gly | Phe | Gly | Ile | Met | Ser | Gly | Val | Phe | Ser | Phe | Val | Asn |
| | | | | 125 | | | | | 130 | | | | | 135 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Ser | Asp | Ser | Leu | Gly | Pro | Gly | Thr | Val | Gly | Ile | His | Gly |
| | | | | 140 | | | | | 145 | | | | | 150 |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ser | Pro | Gln | Phe | Phe | Leu | Tyr | Ser | Ala | Phe | Met | Thr | Leu | Val |
| | | | | 155 | | | | | 160 | | | | | 165 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ile | Leu | Leu | His | Val | Phe | Trp | Gly | Ile | Val | Phe | Phe | Asp | Gly |
| | | | | 170 | | | | | 175 | | | | | 180 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Glu | Lys | Lys | Lys | Trp | Gly | Ile | Leu | Leu | Ile | Val | Leu | Leu | Thr |
| | | | | 185 | | | | | 190 | | | | | 195 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Leu | Leu | Val | Ser | Ala | Gln | Thr | Phe | Ile | Ser | Ser | Tyr | Tyr | Gly |
| | | | | 200 | | | | | 205 | | | | | 210 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Asn | Leu | Ala | Ser | Ala | Phe | Ile | Ile | Leu | Val | Leu | Met | Gly | Thr |
| | | | | 215 | | | | | 220 | | | | | 225 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ala | Phe | Leu | Ala | Ala | Gly | Gly | Ser | Cys | Arg | Ser | Leu | Lys | Leu |
| | | | | 230 | | | | | 235 | | | | | 240 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Leu | Leu | Cys | Gln | Asp | Lys | Asn | Phe | Leu | Leu | Tyr | Asn | Gln | Arg |
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Ser Arg

411 - 225

11 549
11 DNA
11 Homo sapiens

11 226

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Gln | Phe | Gln | Arg | Thr | Tyr | Val | Asp | Gln | Val | Asn | Ser | |
| | | | 35 | | | | | 41 | | | | | 45 | |
| Leu | Val | Asn | Ile | Tyr | Thr | Phe | Asn | His | Thr | Val | Thr | Arg | Asn | |
| | | | 50 | | | | | 55 | | | | | 60 | |
| Thr | Thr | Gln | Gly | Val | Arg | Val | Ser | Val | Asn | Val | Leu | Asn | Lys | Gln |
| | | | 65 | | | | | 70 | | | | | | 75 |
| Lys | Gly | Ala | Pro | Leu | Leu | Phe | Val | Val | Arg | Gln | Lys | Glu | Ala | Val |
| | | | 80 | | | | | | 85 | | | | | 90 |
| Val | Ser | Phe | Gln | Val | Pro | Leu | Ile | Leu | Arg | Gly | Met | Phe | Gln | Arg |
| | | | 95 | | | | | | 100 | | | | | 105 |
| Lys | Tyr | Leu | Tyr | Gln | Lys | Val | Glu | Arg | Thr | Leu | Cys | Gln | Pro | Pro |
| | | | 110 | | | | | | 115 | | | | | 120 |
| Thr | Lys | Asn | Glu | Ser | Glu | Ile | Gln | Phe | Phe | Tyr | Val | Asp | Val | Ser |
| | | | 125 | | | | | | 130 | | | | | 135 |
| Thr | Leu | Ser | Pro | Val | Asn | Thr | Thr | Tyr | Gln | Leu | Arg | Val | Ser | Arg |
| | | | 140 | | | | | | 145 | | | | | 150 |
| Met | Asp | Asp | Phe | Val | Leu | Arg | Thr | Gly | Glu | Gln | Phe | Ser | Phe | Asn |
| | | | 155 | | | | | | 160 | | | | | 165 |
| Thr | Thr | Ala | Ala | Gln | Pro | Gln | Tyr | Phe | Lys | Tyr | Glu | Phe | Pro | Gln |
| | | | 170 | | | | | | 175 | | | | | 180 |
| Gly | Val | Asp | Ser | Val | Ile | Val | Lys | Val | Thr | Ser | Asn | Lys | Ala | Phe |
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| Pro | Cys | Ser | Val | Ile | Ser | Ile | Gln | Asp | Val | Leu | Cys | Pro | Val | Tyr |
| | | | 200 | | | | | | 205 | | | | | 210 |
| Asp | Leu | Asp | Asn | Asn | Val | Ala | Phe | Ile | Gly | Met | Tyr | Gln | Thr | Met |
| | | | 215 | | | | | | 220 | | | | | 225 |
| Thr | Lys | Lys | Ala | Ala | Ile | Thr | Val | Gln | Arg | Lys | Asp | Phe | Pro | Ser |
| | | | 230 | | | | | | 235 | | | | | 240 |
| Asn | Ser | Phe | Tyr | Val | Val | Val | Val | Val | Lys | Thr | Glu | Asp | Gln | Ala |
| | | | 245 | | | | | | 250 | | | | | 255 |
| Cys | Gly | Gly | Ser | Leu | Pro | Phe | Tyr | Pro | Phe | Ala | Glu | Asp | Glu | Pro |
| | | | 260 | | | | | | 265 | | | | | 270 |
| Val | Asp | Gln | Gly | His | Arg | Gln | Lys | Thr | Leu | Ser | Val | Leu | Val | Ser |
| | | | 275 | | | | | | 280 | | | | | 285 |
| Gln | Ala | Val | Thr | Ser | Glu | Ala | Tyr | Val | Ser | Gly | Met | Leu | Phe | Cys |
| | | | 290 | | | | | | 295 | | | | | 300 |
| Leu | Gly | Ile | Phe | Leu | Ser | Phe | Tyr | Leu | Leu | Thr | Val | Leu | Leu | Ala |
| | | | 305 | | | | | | 310 | | | | | 315 |
| Cys | Thr | His | Asn | Thr | Arg | Gln | Lys | Lys | Lys | Thr | Leu | Leu | Val | Ala |

| | | |
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| 335 | 340 | 345 |
| Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly | | |
| 350 | 355 | 360 |
| Asn Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser | | |
| 365 | 370 | 375 |
| Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe | | |
| 380 | 385 | 390 |
| Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val | | |
| 395 | 400 | 405 |
| Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys | | |
| 410 | 415 | 420 |
| Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala | | |
| 425 | 430 | 435 |
| Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe | | |
| 440 | 445 | 450 |
| Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val | | |
| 455 | 460 | 465 |
| Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn | | |
| 470 | 475 | 480 |
| Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly | | |
| 485 | 490 | 495 |
| Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile | | |
| 500 | 505 | 510 |
| Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile | | |
| 515 | 520 | 525 |
| Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu | | |
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| Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr | | |
| 545 | 550 | 555 |
| Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys | | |
| 560 | 565 | 570 |
| Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met | | |
| 575 | 580 | 585 |
| Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro | | |
| 590 | 595 | 600 |
| Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile | | |
| 605 | 610 | 615 |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
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| 635 | | | | | | | | | | | | | | |
| 640 | Ala | Ile | Trp | Ile | Val | Ile | Ser | Ile | Ile | His | Ile | Ile | Ala | Thr |
| 645 | | | | | | | | | | | | | | |
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| 655 | | | | | | | | | | | | | | |
| 660 | Ser | Gly | Ile | Phe | Arg | Arg | Ile | Leu | His | Val | Leu | Tyr | Thr | Asp |
| 665 | | | | | | | | | | | | | | |
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| 675 | | | | | | | | | | | | | | |
| 680 | Leu | Val | Met | Gly | Asn | Val | Ile | Asn | Trp | Ser | Leu | Ala | Ala | Tyr |
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| 690 | Gly | Ile | Ile | Met | Arg | Pro | Asn | Asp | Phe | Ala | Ser | Tyr | Leu | Ala |
| 695 | | | | | | | | | | | | | | |
| 700 | Ile | Gly | Ile | Cys | Asn | Leu | Leu | Leu | Tyr | Phe | Ala | Phe | Tyr | Ile |
| 705 | | | | | | | | | | | | | | |
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| 715 | | | | | | | | | | | | | | |
| 720 | Cys | Ile | Val | Cys | Thr | Ser | Val | Val | Trp | Gly | Phe | Ala | Leu | Phe |
| 725 | | | | | | | | | | | | | | |
| 730 | Phe | Phe | Gln | Gly | Leu | Ser | Thr | Trp | Gln | Lys | Thr | Pro | Ala | Glu |
| 735 | | | | | | | | | | | | | | |
| 740 | Arg | Glu | His | Asn | Arg | Asp | Cys | Ile | Leu | Leu | Asp | Phe | Phe | Asp |
| 745 | | | | | | | | | | | | | | |
| 750 | His | Asp | Ile | Trp | His | Phe | Leu | Ser | Ser | Ile | Ala | Met | Phe | Gly |
| 755 | | | | | | | | | | | | | | |
| 760 | Phe | Leu | Val | Leu | Leu | Thr | Leu | Asp | Asp | Asp | Leu | Asp | Thr | Val |
| 765 | | | | | | | | | | | | | | |
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ctcttctt tctctgccc agctcttc caggtcttc tggagtc 200

24

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| Pro His Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp | 50 | 55 | 60 |
| His Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser | 65 | 70 | 75 |
| Tyr Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala | 80 | 85 | 90 |
| Gln Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val | 95 | 100 | 105 |
| Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn | 110 | 115 | 120 |
| Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu | 125 | 130 | 135 |
| Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala | 140 | 145 | 150 |
| Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe | 155 | 160 | 165 |
| His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe | 170 | 175 | 180 |
| Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly | 185 | 190 | 195 |
| Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu | 200 | 205 | 210 |
| Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala | 215 | 220 | 225 |
| Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser | 230 | 235 | 240 |
| Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro | 245 | 250 | 255 |
| His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr | 260 | 265 | 270 |
| His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu | 275 | 280 | 285 |
| Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala | 290 | 295 | 300 |
| Gln Tyr Leu Leu His Val Arg Ala Gln Asn Ser His Gly His Asp | 305 | 310 | 315 |

| | | | | | | | | | | | | | | |
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| Arg | Val | Ile | Ile | Cys | Pro | Ile | Asn | Asp | Ile | Thr | Val | Ser | Ile | 341 |
| Pro | Leu | Leu | Ser | Pro | Pro | Gly | Thr | Glu | Val | Thr | Arg | Leu | Ser | 360 |
| Glu | Asp | Ala | Asp | Ala | Pro | Gly | Ser | Pro | Asn | Ser | His | Val | Val | 371 |
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| Pro | Leu | Arg | Ala | Gly | Gln | Asn | Ile | Leu | Leu | Leu | Val | Leu | Ala | 410 |
| Asp | Leu | Ala | Gly | Ala | Glu | Gly | Gly | Phe | Ser | Ser | Thr | Cys | Glu | 425 |
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| Thr | Ser | Gln | Ile | Gly | Pro | Ile | Ser | Ile | Pro | Glu | Asp | Val | Glu | 455 |
| Gly | Thr | Leu | Val | Ala | Met | Leu | Thr | Ala | Ile | Asp | Ala | Asp | Leu | 470 |
| Pro | Ala | Phe | Arg | Leu | Met | Asp | Phe | Ala | Ile | Glu | Arg | Gly | Asp | 485 |
| Glu | Gly | Thr | Phe | Gly | Leu | Asp | Trp | Glu | Pro | Asp | Ser | Gly | His | 500 |
| Arg | Leu | Arg | Leu | Cys | Lys | Asn | Leu | Ser | Tyr | Glu | Ala | Ala | Pro | 515 |
| His | Glu | Val | Val | Val | Val | Val | Gln | Ser | Val | Ala | Lys | Leu | Val | 530 |
| Pro | Gly | Pro | Gly | Pro | Gly | Ala | Thr | Ala | Thr | Val | Thr | Val | Leu | 545 |
| Glu | Arg | Val | Met | Pro | Pro | Pro | Lys | Leu | Asp | Gln | Glu | Ser | Tyr | 560 |
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| Ile | Gln | Pro | Ser | Asp | Pro | Ile | Ser | Arg | Thr | Leu | Arg | Phe | Ser | 590 |
| Val | Ala | Asp | Pro | Gln | Gly | Trp | Leu | Cys | Ile | Ala | Lys | Phe | Ser | 605 |

| | | |
|---|-----|-----|
| 620 | 625 | 630 |
| Val His Thr Ala Gln Ser Leu His Gly Ala Gln Pro Gly Asp | | |
| 635 | 640 | 645 |
| Thr Lys Thr Val Leu Val Gln Ala Gln Asp Thr Ala Leu Thr Leu | | |
| 650 | 655 | 660 |
| Gln Pro Val Pro Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His | | |
| 665 | 670 | 675 |
| Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser | | |
| 680 | 685 | 690 |
| Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val | | |
| 695 | 700 | 705 |
| Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr | | |
| 710 | 715 | 720 |
| Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile | | |
| 725 | 730 | 735 |
| Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val | | |
| 740 | 745 | 750 |
| Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg | | |
| 755 | 760 | 765 |
| Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val | | |
| 770 | 775 | 780 |
| Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile | | |
| 785 | 790 | 795 |
| Leu Ile Phe Thr His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp | | |
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 Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
 35 40 45
 Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
 50 55 60
 Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
 65 70 75
 Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
 80 85 90
 Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
 95 100 105
 Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
 110 115 120
 Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
 125 130 135
 Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
 140 145 150
 His Ser Ile Gln Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
 155 160 165

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Tyr

210 - 225
 221 - 1743
 222 - 11A
 223 - 11A

[illegible]

| | | |
|---|-----|-----|
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| His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn | | |
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| Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe | | |
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| Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala | | |
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| Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys | | |
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| Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser | | |
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| Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser | | |
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| Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile | | |
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| 380 | 385 | 390 |
| Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile | | |
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4415 DNA
4416 Artificial

4420
4421 Artificial Sequence
4422 1-34
4423 Synthetic construct.

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
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| | | | | 305 | | | | | 310 | | | | | 315 | |
| Thr | Asn | Ser | Asp | Ser | Ser | Thr | Thr | Ser | Ser | Gly | Ala | Gly | Thr | Ala | |
| | | | | 320 | | | | | 325 | | | | | 330 | |
| Thr | Asn | Ser | Glu | Ser | Ser | Thr | Val | Ser | Ser | Gly | Ile | Ser | Thr | Val | |
| | | | | 335 | | | | | 340 | | | | | 345 | |
| Thr | Asn | Ser | Glu | Ser | Ser | Thr | Pro | Ser | Ser | Gly | Ala | Asn | Thr | Ala | |
| | | | | 350 | | | | | 355 | | | | | 360 | |
| Thr | Asn | Ser | Glu | Ser | Ser | Thr | Thr | Ser | Ser | Gly | Ala | Asn | Thr | Ala | |

| | 365 | 370 | 375 |
|---|-----|-----|-----|
| Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala | 380 | 385 | 390 |
| Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala | 395 | 400 | 405 |
| Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala | 410 | 415 | 420 |
| Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala | 425 | 430 | 435 |
| Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val | 440 | 445 | 450 |
| Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala | 455 | 460 | 465 |
| Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala | 470 | 475 | 480 |
| Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala | 485 | 490 | 495 |
| Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile | 500 | 505 | 510 |
| Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe | 515 | 520 | 525 |
| Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn | 530 | 535 | 540 |
| Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly | 545 | 550 | 555 |
| Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro | 560 | 565 | 570 |
| Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile | 575 | 580 | 585 |
| Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro | 590 | 595 | |

6110 - 244

6111 - 26

6112 - PNA

6113 - Artificial

6220 -

6221 - Artificial Sequence

6222 - 1-26

6223 - Synthetic construct

6400 - 244

ctgttggg gggatggtt gggatggtt gggatggtt gggatggtt 700
 gggatggtt gggatggtt gggatggtt gggatggtt gggatggtt 750
 gggatggtt gggatggtt gggatggtt gggatggtt gggatggtt 800
 gggatggtt gggatggtt gggatggtt gggatggtt gggatggtt 850
 gggatggtt gggatggtt gggatggtt gggatggtt gggatggtt 900
 gggatggtt gggatggtt gggatggtt gggatggtt gggatggtt 950
 gggatggtt 957

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 <211> 247
 <212> FRT
 <213> Homo sapiens

<400> 248
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 Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu
 20 25 30
 Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg
 35 40 45
 Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
 50 55 60
 Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
 65 70 75
 Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
 80 85 90
 Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
 95 100 105
 Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
 110 115 120
 Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
 125 130 135
 Gly Ile His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
 140 145 150
 Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
 155 160 165
 Val Gln Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala
 170 175 180

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Lys | Glu | Met | His | Asn | Ala | His | Asn | Gly | Val | Asn | Gln | Ala | Ser |
| | | | | | 195 | | | | 196 | | | | | 197 |
| Lys | Glu | Ala | Asn | Gln | Leu | Leu | Asn | Gly | Asn | His | Gln | Ser | Gly | Ser |
| | | | 200 | | | | | | 205 | | | | | 210 |
| Ser | Ser | His | Gln | Gly | Gly | Ala | Thr | Thr | Thr | Pro | Leu | Ala | Ser | Gly |
| | | | 215 | | | | | | 220 | | | | | 225 |
| Ala | Ser | Val | Asn | Thr | Pro | Phe | Ile | Asn | Leu | Pro | Ala | Leu | Trp | Arg |
| | | | 230 | | | | | | 235 | | | | | 240 |
| Ser | Val | Ala | Asn | Ile | Met | Pro | | | | | | | | |
| | | | 245 | | | | | | | | | | | |

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<230> 249

<231> catat'gat attgcacgtc tgg 23

<240> 250

<241> 24

<242> DNA

<243> Artificial

<250>

<251> Artificial Sequence

<252> 1-4

<253> Synthetic construct.

<260> 250

<261> aaagcttctt gcttccttct ctgc 24

<270> 251

<271> 43

<272> DNA

<273> Artificial

<280>

<281> Artificial Sequence

<282> 1-43

<283> Synthetic construct.

<290> 251

<291> taccacatt gagaaggtca ttaaagggat caacagaggg ctg 43

<300> 252

<301> 37-1

<302> DNA

<303> Homo sapiens

33

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Leu | Ser | Ser | Asn | Leu | Ser | Phe | Leu | Pro | Gly | Gly | Gln | Tyr | 111 |
| Ala | Pro | Leu | Leu | Trp | Gly | Ala | Asp | Ala | Glu | Lys | Lys | Gln | Gln | Cys | 116 |
| Pro | Leu | Lys | Gly | Lys | Asp | Pro | Gln | Arg | Asp | Cys | Gln | Asn | Tyr | Ile | 125 |
| Lys | Ile | Leu | Leu | Pro | Leu | Ser | Gly | Ser | His | Leu | Phe | Thr | Cys | Gly | 140 |
| Thr | Ala | Ala | Phe | Ser | Pro | Met | Cys | Thr | Tyr | Ile | Asn | Met | Gln | Asn | 155 |
| Phe | Thr | Leu | Ala | Arg | Asp | Glu | Lys | Gly | Asn | Val | Leu | Leu | Glu | Asp | 170 |
| Gly | Lys | Gly | Arg | Cys | Pro | Phe | Asp | Pro | Asn | Phe | Lys | Ser | Thr | Ala | 185 |
| Leu | Val | Val | Asp | Gly | Glu | Leu | Tyr | Thr | Gly | Thr | Val | Ser | Ser | Phe | 200 |
| Gln | Gly | Asn | Asp | Pro | Ala | Ile | Ser | Arg | Ser | Gln | Ser | Leu | Arg | Pro | 215 |
| Thr | Lys | Thr | Glu | Ser | Ser | Leu | Asn | Trp | Leu | Gln | Asp | Pro | Ala | Phe | 230 |
| Val | Ala | Ser | Ala | Tyr | Ile | Pro | Glu | Ser | Leu | Gly | Ser | Leu | Gln | Gly | 245 |
| Asp | Asp | Asp | Lys | Ile | Tyr | Phe | Phe | Phe | Ser | Glu | Thr | Gly | Gln | Glu | 260 |
| Phe | Glu | Phe | Phe | Glu | Asn | Thr | Ile | Val | Ser | Arg | Ile | Ala | Arg | Ile | 275 |
| Cys | Lys | Gly | Asp | Glu | Gly | Gly | Glu | Arg | Val | Leu | Gln | Gln | Arg | Trp | 290 |
| Thr | Ser | Phe | Leu | Lys | Ala | Gln | Leu | Leu | Cys | Ser | Arg | Pro | Asp | Asp | 305 |
| Gly | Phe | Pro | Phe | Asn | Val | Leu | Gln | Asp | Val | Phe | Thr | Leu | Ser | Pro | 320 |
| Ser | Pro | Gln | Asp | Trp | Arg | Asp | Thr | Leu | Ile | Tyr | Gly | Val | Phe | Thr | 335 |
| Ser | Gln | Trp | His | Arg | Gly | Thr | Thr | Glu | Gly | Ser | Ala | Val | Cys | Val | 350 |
| Phe | Thr | Met | Lys | Asp | Val | Gln | Arg | Val | Phe | Ser | Gly | Leu | Tyr | Lys | 365 |

| | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Asn | Asn | Thr | Gln | Gln | His | Tyr | Thr | Val | Thr | His | Ile |
| 414 | | | | | | | 414 | | | | | |
| Thr | Br | Arg | Ile | Gly | Ala | Tyr | Ile | Thr | Asn | Ser | Ala | Arg |
| 416 | | | | | | | 416 | | | | | 416 |
| Asn | Iys | Ile | Asn | Ser | Ser | Leu | Gln | Leu | Pro | Asp | Arg | Val |
| 418 | | | | | | | 418 | | | | | 418 |
| Asn | Ihe | Leu | Lys | Asp | His | Ihe | Leu | Met | Asp | Gly | Gln | Val |
| 425 | | | | | | | 425 | | | | | 425 |
| Met | Leu | Leu | Leu | Gln | Pro | Gln | Ala | Arg | Tyr | Gln | Arg | Val |
| 440 | | | | | | | 440 | | | | | 440 |
| His | Arg | Val | Pro | Gly | Leu | His | His | Thr | Tyr | Asp | Val | Leu |
| 445 | | | | | | | 445 | | | | | 445 |
| Leu | Gly | Thr | Gly | Asp | Gly | Arg | Leu | His | Lys | Ala | Val | Ser |
| 449 | | | | | | | 449 | | | | | 449 |
| Pro | Arg | Val | His | Ile | Ile | Glu | Glu | Leu | Gln | Ile | Phe | Ser |
| 481 | | | | | | | 481 | | | | | 481 |
| Gln | Pro | Val | Gln | Asn | Leu | Leu | Leu | Asp | Thr | His | Arg | Gly |
| 505 | | | | | | | 505 | | | | | 505 |
| Tyr | Ala | Ala | Ser | His | Ser | Gly | Val | Val | Gln | Val | Pro | Met |
| 511 | | | | | | | 511 | | | | | 511 |
| Cys | Ser | Leu | Tyr | Arg | Ser | Cys | Gly | Asp | Cys | Leu | Leu | Ala |
| 530 | | | | | | | 530 | | | | | 530 |
| Pro | Tyr | Cys | Ala | Trp | Ser | Gly | Ser | Ser | Cys | Lys | His | Val |
| 545 | | | | | | | 545 | | | | | 545 |
| Tyr | Gln | Pro | Gln | Leu | Ala | Thr | Arg | Pro | Trp | Ile | Gln | Asp |
| 560 | | | | | | | 560 | | | | | 560 |
| Gly | Ala | Ser | Ala | Lys | Asp | Leu | Cys | Ser | Ala | Ser | Ser | Val |
| 575 | | | | | | | 575 | | | | | 575 |
| Pro | Ser | Phe | Val | Pro | Thr | Gly | Glu | Lys | Pro | Cys | Glu | Gln |
| 590 | | | | | | | 590 | | | | | 590 |
| Phe | Gln | Pro | Asn | Thr | Val | Asn | Thr | Leu | Ala | Cys | Pro | Leu |
| 605 | | | | | | | 605 | | | | | 605 |
| Asn | Leu | Ala | Thr | Arg | Leu | Trp | Leu | Arg | Asn | Gly | Ala | Pro |
| 620 | | | | | | | 620 | | | | | 620 |
| Ala | Ser | Ala | Ser | Cys | His | Val | Leu | Ile | Thr | Gly | Asp | Leu |
| 635 | | | | | | | 635 | | | | | 635 |
| Val | Gly | Thr | Gln | Gln | Leu | Gly | Gln | Phe | Gln | Cys | Trp | Ser |
| 650 | | | | | | | 650 | | | | | 650 |
| Val | Gly | Phe | Gln | Gln | Leu | Val | Ala | Pro | Tyr | Tyr | Ile | Gln |
| 665 | | | | | | | 665 | | | | | 665 |

| | | |
|-------------------------------------|-------------------------|-----|
| 665 | 675 | 685 |
| Leu Arg Gly Val Ala Arg His Thr Asp | Glu Gly Gly Ser Val Pro | |
| 680 | 685 | 690 |
| Val Ile Ile Ser Thr Ser Arg Val Ser | Ala Pro Ala Gly Gly Lys | |
| 695 | 700 | 705 |
| Ala Ser Trp Gly Ala Asp Arg Ser Tyr | Tyr Lys Glu Phe Leu Val | |
| 710 | 715 | 720 |
| Met Cys Thr Leu Phe Val Leu Ala Val | Leu Leu Pro Val Leu Phe | |
| 725 | 730 | 735 |
| Leu Leu Tyr Arg His Arg Asn Ser Met | Lys Val Phe Leu Lys Glu | |
| 740 | 745 | 750 |
| Gly Glu Cys Ala Ser Val His Pro Lys | Thr Cys Pro Val Val Leu | |
| 755 | 760 | 765 |
| Pro Pro Glu Thr Arg Pro Leu Asn Gly | Leu Gly Pro Pro Ser Thr | |
| 770 | 775 | 780 |
| Pro Leu Asp His Arg Gly Tyr Glu Ser | Leu Ser Asp Ser Pro Pro | |
| 785 | 790 | 795 |
| Gly Ala Arg Val Phe Thr Glu Ser Glu | Lys Arg Pro Leu Ser Ile | |
| 800 | 805 | 810 |
| Glu Asp Ser Phe Val Glu Val Ser Pro | Val Cys Pro Arg Pro Arg | |
| 815 | 820 | 825 |
| Val Arg Leu Gly Ser Glu Ile Arg Asp | Ser Val Val | |
| 830 | 835 | |

6108 254

6111 24

6112 DNA

6113 Artificial

6120

6121 Artificial Sequence

6122 1-24

6123 Synthetic construct.

6400 154

agpccutaca gaattctgctc ctgg 24

6110 255

6111 24

6112 DNA

6113 Artificial

6120

6121 Artificial Sequence

6122 1-24

6123 Synthetic construct.

<215> 256
 <216> 18
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 <218> FNA
 <219> Artificial

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 <222> 1-18
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 <400> 256
 gtacagctg cagttggc 18

 <215> 257
 <216> 41
 <217> DNA
 <218> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-41
 <223> Synthetic construct.

 <400> 257
 atagccatg tgagcaagtc cagttccagc ccaacacagt g 41

 <215> 258
 <216> 45
 <217> DNA
 <218> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

 <400> 258
 gaatttcaga tctttctcgc gggacacccc gtgcagaatc tcttc 45

 <215> 259
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 <218> Homo sapiens

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 <223> unknown base

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 ctatpccaga agatctgcag ctgcggcggc gccgcgggt a taaatga 10

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 tttttttt tggatctg agtctctg cttttctt cttggttt 10

243

tttttttt gttttttt tttttttt tttttttt tttttttt 150
 ttgaggaca ggggggtt ttgaggaa ttgaggaca tttttttt 160
 ttgaggaa ttgttttt ttgttttt ttgttttt ttgttttt 170
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tttttttttt ttt 490

<210> 260

<211> 802

<212> ERT

<213> Homo sapiens

<400> 260

Met Ala Ala Arg Gly Arg Arg Ala Trp Leu Ser Val Leu Leu Gly
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Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg
20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Gln Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Leu | Arg | Glu | Met | Tyr | Thr | Thr | His | Gln | Asp | Val | Glu | Val | 245 | 255 |
| Gly | Arg | Tyr | Val | Arg | Arg | Phe | Ala | Gly | Val | Gln | Cys | Val | Trp | Ser | 260 | 270 |
| Tyr | Gln | Met | Arg | Gln | Leu | Phe | Tyr | Glu | Asn | Tyr | Glu | Gln | Asn | Lys | 275 | 285 |
| Lys | Gly | Tyr | Ile | Arg | Asp | Leu | His | Asn | Ser | Lys | Ile | His | Gln | Ala | 290 | 300 |
| Ile | Thr | Leu | His | Pro | Asn | Lys | Asn | Pro | Pro | Tyr | Gln | Tyr | Arg | Leu | 305 | 315 |
| His | Ser | Tyr | Met | Leu | Ser | Arg | Lys | Ile | Ser | Glu | Leu | Arg | His | Arg | 320 | 330 |
| Thr | Ile | Gln | Leu | His | Arg | Glu | Ile | Val | Leu | Met | Ser | Lys | Tyr | Ser | 335 | 345 |
| Asn | Thr | Glu | Ile | His | Lys | Glu | Asp | Leu | Gln | Leu | Gly | Ile | Pro | Pro | 350 | 360 |
| Ser | Phe | Met | Arg | Phe | Gln | Pro | Arg | Gln | Arg | Glu | Glu | Ile | Leu | Glu | 365 | 375 |
| Trp | Glu | Phe | Leu | Thr | Gly | Lys | Tyr | Leu | Tyr | Ser | Ala | Val | Asp | Gly | 380 | 390 |
| Gln | Pro | Pro | Arg | Arg | Gly | Met | Asp | Ser | Ala | Gln | Arg | Glu | Ala | Leu | 395 | 405 |
| Asp | Asp | Ile | Val | Met | Gln | Val | Met | Glu | Met | Ile | Asn | Ala | Asn | Ala | 410 | 420 |
| Lys | Thr | Arg | Gly | Arg | Ile | Ile | Asp | Phe | Lys | Glu | Ile | Gln | Tyr | Gly | 425 | 435 |
| Tyr | Arg | Arg | Val | Asn | Pro | Met | Tyr | Gly | Ala | Glu | Tyr | Ile | Leu | Asp | 440 | 450 |
| Leu | Leu | Leu | Leu | Tyr | Lys | Lys | His | Lys | Gly | Lys | Lys | Met | Thr | Val | 455 | 465 |
| Pro | Val | Arg | Arg | His | Ala | Tyr | Leu | Gln | Gln | Thr | Phe | Ser | Lys | Ile | 470 | 480 |
| Gln | Phe | Val | Glu | His | Glu | Glu | Leu | Asp | Ala | Gln | Glu | Leu | Ala | Lys | 485 | 495 |
| Arg | Ile | Asn | Gln | Glu | Ser | Gly | Ser | Leu | Ser | Phe | Leu | Ser | Asn | Ser | 500 | 510 |
| Leu | Lys | Lys | Leu | Val | Pro | Phe | Gln | Leu | Pro | Gly | Ser | Lys | Ser | Glu | 515 | 525 |
| His | Lys | Gln | Pro | Lys | Asp | Lys | Lys | Ile | Asn | Ile | Leu | Ile | Pro | Leu | | |

| | | |
|-------------------------------------|-------------------------|-----|
| 532 | 535 | 540 |
| Ser Gly Arg Phe Asp Met Ile Val Arg | Phe Met Gly Asn Phe Glu | |
| 545 | 550 | 555 |
| Lys Thr Cys Leu Ile Pro Asn Gln Asn | Val Lys Leu Val Val Leu | |
| 560 | 565 | 570 |
| Leu Phe Asn Ser Asp Ser Asn Pro Asp | Lys Ala Lys Gln Val Glu | |
| 575 | 580 | 585 |
| Leu Met Arg Asp Tyr Arg Ile Lys Tyr | Pro Lys Ala Asp Met Glu | |
| 590 | 595 | 600 |
| Ile Leu Pro Val Ser Gly Glu Phe Ser | Arg Ala Leu Ala Leu Glu | |
| 605 | 610 | 615 |
| Val Gly Ser Ser Gln Phe Asn Asn Glu | Ser Leu Leu Phe Phe Cys | |
| 620 | 625 | 630 |
| Asp Val Asp Leu Val Phe Thr Thr Glu | Phe Leu Gln Arg Cys Arg | |
| 635 | 640 | 645 |
| Ala Asn Thr Val Leu Gly Gln Gln Ile | Tyr Phe Pro Ile Ile Phe | |
| 650 | 655 | 660 |
| Ser Gln Tyr Asp Pro Lys Ile Val Tyr | Ser Gly Lys Val Pro Ser | |
| 665 | 670 | 675 |
| Asp Asn His Phe Ala Phe Thr Gln Lys | Thr Gly Phe Trp Arg Asn | |
| 680 | 685 | 690 |
| Tyr Gly Phe Gly Ile Thr Cys Ile Tyr | Lys Gly Asp Leu Val Arg | |
| 695 | 700 | 705 |
| Val Gly Gly Phe Asp Val Ser Ile Gln | Gly Trp Gly Leu Glu Asp | |
| 710 | 715 | 720 |
| Val Asp Leu Phe Asn Lys Val Val Gln | Ala Gly Leu Lys Thr Phe | |
| 725 | 730 | 735 |
| Arg Ser Gln Glu Val Gly Val Val His | Val His His Pro Val Phe | |
| 740 | 745 | 750 |
| Cys Asp Pro Asn Leu Asp Pro Lys Gln | Tyr Lys Met Cys Leu Gly | |
| 755 | 760 | 765 |
| Ser Lys Ala Ser Thr Tyr Gly Ser Thr | Gln Gln Leu Ala Glu Met | |
| 770 | 775 | 780 |
| Trp Leu Glu Lys Asn Asp Pro Ser Tyr | Ser Lys Ser Ser Asn Asn | |
| 785 | 790 | 795 |
| Asn Gly Ser Val Arg Thr Ala | | |
| 800 | | |

<210> 261

<211> 24

<211> tNA
<213> Artificial

<215>
<217> Artificial Sequence
<220> 1-24
<223> Synthetic construct.

<400> 261
tgcacactac ggggtgtgga cgac 24

<210> 262
<211> 24
<213> tNA
<215> Artificial

<215>
<217> Artificial Sequence
<220> 1-24
<223> Synthetic construct.

<400> 162
tgcatttct tccgtggtgc ccag 24

<210> 263
<211> 1
<213> DNA
<215> Artificial

<215>
<217> Artificial Sequence
<220> 1-46
<223> Synthetic construct.

<400> 265
ccagaadaag tcttcatga tgcacaagta catgcacac cactac 46

<210> 264
<211> 1419
<213> DNA
<215> Homo sapiens

<400> 264
ggacaaccgt tcttgggtgt cccagggcct gaggcaggac ggtactccgc 50
tgacaacctt cctttcgggc ttgaggttcc cagcctgggtg gcccaggac 100
gttccggtcg catggcagag tgcacggac gacgcctatg aagcccttag 150
tctttctagt tgcctttttg ctatggcctt cgtctgtgac ggcttatecg 200
apcataactg tgacacctga tgaagagaaa caactgaatc attatataca 250
agttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaatac caactctgca aaactgtgtt attctatac atcaaaaagg 350
tcaacttita agagctagt taccataga aactttta tgaactaga 400

| | | |
|---|-----|-----|
| 110 | 115 | 120 |
| His Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys | | |
| 81 | 71 | 75 |
| Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu | | |
| 86 | 75 | 90 |
| Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly | | |
| 95 | 100 | 105 |
| Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro | | |
| 110 | 115 | 120 |
| Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala | | |
| 125 | 130 | 135 |
| Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu | | |
| 140 | 145 | 150 |
| Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val | | |
| 155 | 160 | 165 |
| Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro | | |
| 170 | 175 | 180 |
| Val Phe Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Gln | | |
| 185 | 190 | 195 |
| Ser Glu Asp Val Pro Gln Leu Ser Gly Gln Thr Ala Ile Glu Lys | | |
| 200 | 205 | 210 |
| Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp | | |
| 215 | 220 | 225 |
| Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala | | |
| 230 | 235 | 240 |
| Leu Leu Ser Asp Thr Ser Asn Pro Ala Thr Arg Glu Asp Ile Glu | | |
| 245 | 250 | 255 |
| Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala | | |
| 260 | 265 | 270 |
| Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro | | |
| 275 | 280 | 285 |
| Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Phe Val Ile | | |
| 290 | 295 | 300 |
| Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp | | |
| 305 | 310 | 315 |
| Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val | | |
| 320 | 325 | 330 |
| Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala | | |
| 335 | 340 | 345 |

Leu Leu Lys Val Tyr
310

<110> 266

<211> 2403

<212> FNA

<213> Homo sapiens

<400> 266

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acagctggcc taactccaa atcatccatc taccctctct gtcctctatt 100
ttcatagtat gagatccac ccacaggaata tccatggctt ttgtgctcat 150
tttggttctc agttttctac auctgggttc aatcagttc caactcactg 200
gaacggggcaa gtttgtccag gcttgggtgg gaaagacac cgtgttctcc 250
tgtccctctt ttctcgagac cagtgcagag gctatggaag tgggttcttt 300
caggaatcag ttcatgctt tggctccact ctacagagat ggggaagact 350
gggaatctaa gcagatgcca cagtatcgag ggagaaactg gtttgtgaag 400
gaatccattg caggggggca tctctctta agcttaaaa acatccctcc 450
ctcggacatc ggctgttat ggtgctgatt cagttccag atttaagata 500
aggaggccac ctggagctg cagggggag cactggctc acttcccttc 550
atttccatcc tgggataagt tgaaggaggt atccagttac tctgctgttc 600
ctcaggtctg ttcccccag ccacagccaa gtggaaaggt ccacaaggac 650
aggatttctc ttcagactcc agagccaatg cagatcgcta cagcctgtat 700
gatgtggaga tctccattat agtccaggaa aatgctggga ccataattgtg 750
ttccatccac ctgtctgagc agagtcatt ga ggtggaaacc aaggtattga 800
taggagagac gtttttccag cctccactt ggccctggc ttctatttta 850
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tgttttcttc aaatccaaag gaaaaatcca ggcgggaactg caactggagaa 950
gaaagcacgg acaggccagaa ttgagagacg ccccgaaaca cgcattugan 1000
gtgactctgg atccagagac ggtccacccg aactctctgg tttctgactc 1050
gaaaactufa acccatagaa aaatcccca ggaagtggct tactctgaga 1100
agacattta aaggaagact gtgtggctt ctcaggtttt ccaagcagga 1150
aacatttact agagattca cctccagaaa aatgtaggat ctctcttcca 1200
attgtgtgtg atccgctac atcccccaa gaaactgtg attttctctc 1250

ccacaaatgg atatttggtc ctacagctta caacagatca ttttttttt 1300
 acatttcatt tttattttat cagctctccc cccagcagac ctgctacag 1350
 agtaggggtc ttcttgaact atcaggggtg gaccatctcc ttcttcaata 1400
 caaatgacaa gttccttatt tataccctgc taccatgt ca gtttgaaagg 1450
 ttgttgaaac cctatatcca gcatgggatg tatgaaggag aaaaggggac 1500
 ccccatattc atatgtccag tgtcctgggg atcaaacaaa gaagaccctg 1550
 ctttaaggga cccacacac agacacagac acagcagagg gagagtgtc 1600
 ccgacaggtc ccccagctt cctctccgga gcttgagcac agagagt ca 1650
 gcccccact ctcttttagg gagctjaagt tcttctgccc tgagcctgc 1700
 agcaggggca gtcacagctt ccagatgagg ggggatttgc ctgaccctgt 1750
 gggagtccaa agccatggct gccctjaagt ggggaggga tagactcaca 1800
 ctaggtttag ttgtgaaaa ctcctccag ctaaggatc ttgaacaaqt 1850
 cacaacctcc caggtcctc atttctagt caccgacagt gattcctgc 1900
 ccacaggtga agattaaaga gacaacgaat ghaatcctg cttgaggtt 1950
 tgagggcaca ggtttgtc atgatgtgt tttatttat acattttccc 2000
 accataact ctgtttgctt attccacatt aaattacttt tctctatac 2050
 aaatccccca tggaaatagt attgaacac tcttttgtga ggtccaaaa 2100
 ataaagagga ggtaggattt ttaactgatt ctataagccc agcattacct 2150
 gatacaaaaa ccaggcaag aaaacagaag aagaggaagg aaactacag 2200
 gtcatactcc ctcattaaca cagacacaaa aattctaaat aaaattttta 2250
 caatttaaac taacaaat atttaaaat gatataaac tactcagtgt 2300
 ggtttgtccc acaaatgcag agttggttta atatttaaat atcaaccagt 2350
 gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400
 aaa 2403

C110 - 267
 C111 - 466
 C112 - PRT
 C113 - Homo sapiens

<400> 267
 Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Gln Leu Val
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 Ser Gly Gln Tyr Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Ile Glu
45 45 45

Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe
50 55 60

His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser
65 70 75

Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp
80 85 90

Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr
95 100 105

Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile
110 115 120

Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly
125 130 135

Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile
140 145 150

Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala
155 160 165

Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg
170 175 180

Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile
185 190 195

Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu
200 205 210

Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu
215 220 225

Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu
230 235 240

Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile
245 250 255

Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp
260 265 270

Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys
275 280 285

His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys
290 295 300

Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro
305 310 315

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Gln | Val | Ile | His | Ser | Gln | Lys | Arg | Phe | Thr | Arg | Lys | Ser | Val | 320 | 330 |
| Val | Ala | Ser | Gln | Gly | Phe | Gln | Ala | Gly | Arg | His | Tyr | Trp | Glu | Val | 335 | 345 |
| Asp | Val | Gly | Gln | Asn | Val | Gly | Trp | Tyr | Val | Gly | Val | Cys | Arg | Asp | 350 | 360 |
| Asp | Val | Asp | Arg | Gly | Lys | Asn | Asn | Val | Thr | Leu | Ser | Pro | Asn | Asn | 365 | 375 |
| Gly | Tyr | Trp | Val | Leu | Arg | Leu | Thr | Thr | Glu | His | Leu | Tyr | Phe | Thr | 380 | 390 |
| Phe | Asn | Pro | His | Phe | Ile | Ser | Leu | Pro | Pro | Ser | Thr | Pro | Pro | Thr | 395 | 405 |
| Arg | Val | Gly | Val | Phe | Leu | Asp | Tyr | Glu | Gly | Gly | Thr | Ile | Ser | Phe | 410 | 420 |
| Phe | Asn | Thr | Asn | Asp | Gln | Ser | Leu | Ile | Tyr | Thr | Leu | Leu | Thr | Cys | 425 | 435 |
| Gln | Phe | Glu | Gly | Leu | Leu | Arg | Pro | Tyr | Ile | Gln | His | Ala | Met | Tyr | 440 | 450 |
| Asp | Gln | Glu | Lys | Gly | Thr | Pro | Ile | Phe | Ile | Cys | Pro | Val | Ser | Trp | 455 | 465 |

Gly

c2100: 168
 c2110: 2103
 c2120: DNA
 c2130: Homo sapiens

c400: 168
 gcttccacagg actcttcatt gctggttggc aatgatgtat cggccagatg 50
 tgggtgagggc taggaaaaga gtttggttggg aaacctgggt tatcggcctc 100
 gtcattctca tatccctgat tgcctggca gtgtgcattg gactcaatgt 150
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcaat 200
 tgtcatttac aactacaaa ctatatgtg aatttggcag agaggcttct 250
 aacaatttta cagaaatgag ccagagaact gaataatgg tgaaaaatgc 300
 attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350
 aattcagaca acagaagcat ggagtgttg ttatatgct gttgatttat 400
 adatttcaat ctactagga tctcgaact ctagataaa ttgttcaact 450
 ttttttaact gaaaagtggc aagatctgt tggcgcact caggttatca 500

ctcaacttgg taaaattttaa aaatcaaaa agaaagaaa aaacacat 550
 cttaaacatt gctggggaac aaaaagaatg aaaaatctag gtaagaatct 600
 caggatcatt ggtgggacag aagtagaaca gggtaaatgg ccttggaagg 650
 ctaggctgca gtgggatggg actcatcact gtggagcaac cttaattaat 700
 gccacatggc ttgtgagtgc tgcacactgt tttaaacat ataagaaccc 750
 tgcacatggc actgcttctt ttgagtaac aataaaact ctgaaatga 800
 aagggggtct caggagaata attgttcatg aaaaatataa aaacacatca 850
 catgactatg atattttctt tgcagagctt tctaggcttg ttcctacac 900
 aaatgcagta catagagttt ctctcctga tgcacatct gagtttcaac 950
 caggtgatgt gatgtttgtg acaggatttg gagcactgaa aaatgatgg 1000
 tacagtcaaa atcatcttgc acaagcacaq gtgactctca tagacgctac 1050
 aacttgcaat gaacctcag cttaaatga cgcataact cctagaatgt 1100
 tatgtgctgg ctcttagaa ggaaaaacag atgcatgca gggtagctct 1150
 ggaggacac cggttagtto agatgctaga gatctctggc aacttgctgg 1200
 aatagtgaac tggggagatg atgtgcgaa acacaacaag cctgggtgtt 1250
 atactagagt taaggccttg cgggactgca ttaactcaaa aactggatat 1300
 taagagacaa aagcctcatg gaacagataa catttttttt tgtttttgg 1350
 gtgtggaggo catttttaga gatacagaat tggagaagac ttgcaaaaac 1400
 gctagatttg actgatctca ataaactgtt tgcctgatgc atgtatttt 1450
 ttcacagctc tgttcgac gttagcatcc tgcctctgac agatcaactc 1500
 tgcacatctg gagcaatagt tgaacttta tgtacataga gaatagata 1550
 atacaatatt acattacagc ctgtattcat ttgtctctca gaagtttgt 1600
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 agcaactcct ttcttcagtt cctcagctcc tctcatttca gcaaatatcc 1700
 attttcaagg tgcagacaa ggaagtgaag aaaaataag aagaaaaaaa 1750
 tccctacat ttattggca cagaaaagta ttaggtgttt ttcttagtgc 1800
 aatattagaa atgacatat tcattatcaa aggtcaagca aagacagcag 1850
 aatcaaatc acttcatcct ttggaanta tgggaanta attaaggaa 1900
 tcaaaaaa agcaaatata tatcttatt ttcatctca aaacataat 1950

atgataatg taaadaagat tctgttttt ttgtgacctat aataatata 2070
 caaatctaat gcaatgtact tcttctatgc aaatttaagc aaatatttat 2080
 ttaacattgt tactgaggat gtaacatat aacaataaaa tataaatcac 2100
 caa 2103

<210> 269
 <211> 423
 <212> PBT
 <213> Homo sapiens

<400> 269
 Met Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys
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 Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile
 20 25 30
 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
 110 115 120
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
 155 160 165
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 215 220 225

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|-----|-----|
| Trp | Leu | Val | Ser | Ala | Ala | His | Cys | Phe | Thr | Thr | Tyr | Lys | Asn | Pro | | 230 | 235 | 240 |
| Ala | Arg | Trp | Thr | Ala | Ser | Phe | Gly | Val | Thr | Ile | Lys | Pro | Ser | Lys | | 245 | 250 | 255 |
| Met | Lys | Arg | Gly | Leu | Arg | Arg | Ile | Ile | Val | His | Glu | Lys | Tyr | Lys | | 260 | 265 | 270 |
| His | Pro | Ser | His | Asp | Tyr | Asp | Ile | Ser | Leu | Ala | Glu | Leu | Ser | Ser | | 275 | 280 | 285 |
| Pro | Val | Pro | Tyr | Thr | Asn | Ala | Val | His | Arg | Val | Cys | Leu | Pro | Asp | | 290 | 295 | 300 |
| Ala | Ser | Tyr | Glu | Phe | Gln | Pro | Gly | Asp | Val | Met | Phe | Val | Thr | Gly | | 305 | 310 | 315 |
| Phe | Gly | Ala | Leu | Lys | Asn | Asp | Gly | Tyr | Ser | Gln | Asn | His | Leu | Arg | | 320 | 325 | 330 |
| Gln | Ala | Gln | Val | Thr | Leu | Ile | Asp | Ala | Thr | Thr | Cys | Asn | Glu | Pro | | 335 | 340 | 345 |
| Gln | Ala | Tyr | Asn | Asp | Ala | Ile | Thr | Pro | Arg | Met | Leu | Cys | Ala | Gly | | 350 | 355 | 360 |
| Ser | Leu | Glu | Gly | Lys | Thr | Asp | Ala | Cys | Gln | Gly | Asp | Ser | Gly | Gly | | 365 | 370 | 375 |
| Pro | Leu | Val | Ser | Ser | Asp | Ala | Arg | Asp | Ile | Trp | Tyr | Leu | Ala | Gly | | 380 | 385 | 390 |
| Ile | Val | Ser | Trp | Gly | Asp | Glu | Cys | Ala | Lys | Pro | Asn | Lys | Pro | Gly | | 395 | 400 | 405 |
| Val | Tyr | Thr | Arg | Val | Thr | Ala | Leu | Arg | Asp | Trp | Ile | Thr | Ser | Lys | | 410 | 415 | 420 |

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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cagacgtcag ctgggtggatt cccgtgtcat caaggcctac ccaatgtctc 150

gatgttggg totctcttgc ttctgtggat cctggccttc acctctcttg 200

ttccagagac tcaatctctg tccctcagg attttcaga ccagatgaca 250

gatgagaatg agacagagtg gacgacttg cagctgtac catgagacta 300
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jaacccggga gaatgggaga agtgagcatt ggggcagaag agggccggga 450
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ttaaaaaaa aaaaaaaa 1170

<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe
1 5 10 15
Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu
20 25 30
Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
35 40 45
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
50 55 60
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
65 70 75

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Ser | Ser | Pr | Ala | Gln | Pro | Pro | Asp | Pro | Pro | Arg | Met | Gly | Glu | |
| | | | | 80 | | | | | 85 | | | | | 90 | |
| Val | Arg | Ile | Ala | Ala | Glu | Glu | Gly | Arg | Ala | Val | Val | His | Trp | Cys | |
| | | | | 95 | | | | | 100 | | | | | 105 | |
| Ala | Pro | Phe | Ser | Pro | Val | Leu | His | Tyr | Trp | Leu | Leu | Leu | Trp | Asp | |
| | | | | 110 | | | | | 115 | | | | | 120 | |
| Gly | Ser | Glu | Ala | Ala | Gln | Lys | Gly | Pro | Pro | Leu | Asn | Ala | Thr | Val | |
| | | | | 125 | | | | | 130 | | | | | 135 | |
| Arg | Arg | Ala | Glu | Leu | Lys | Gly | Leu | Lys | Pro | Gly | Gly | Ile | Tyr | Val | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Val | Cys | Val | Val | Ala | Ala | Asn | Glu | Ala | Gly | Ala | Ser | Arg | Val | Pro | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Gln | Ala | Gly | Gly | Glu | Gly | Leu | Glu | Gly | Ala | Asp | Ile | Pro | Ala | Phe | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| Gly | Pro | Cys | Ser | Arg | Leu | Ala | Val | Pro | Pro | Asn | Pro | Arg | Thr | Leu | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Val | His | Ala | Ala | Val | Gly | Val | Gly | Thr | Ala | Leu | Ala | Leu | Leu | Ser | |
| | | | | 200 | | | | | 205 | | | | | 210 | |
| Cys | Ala | Ala | Leu | Val | Trp | His | Phe | Cys | Leu | Arg | Asp | Arg | Trp | Gly | |
| | | | | 215 | | | | | 220 | | | | | 225 | |
| Cys | Pro | Arg | Arg | Ala | Ala | Ala | Arg | Ala | Ala | Gly | Ala | Leu | | | |
| | | | | 230 | | | | | 235 | | | | | | |

c2100 272
 c2110 2397
 c2120 tNA
 c2130 Homo sapiens

c4000 272
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 cgaagaagtt cccgtccccc atgagccccc ggcgtgcgtc cccgactatc 100
 cccaggcggg cgtggggcac cgggccagc gcgacagatc gctgcggttt 150
 tgcctctggg agtaggatgt ggtgaaagga tgggacttct ccttaacggg 200
 gctcacaatg gccagagaag attccgtgaa gtgtctacgc tgcctgctct 250
 accgcctcaa tctgctcttt tggttaatgt ccatcagttg gttggcagtt 300
 tctgcttggg tgagggaact cctaaataat gttctcactt taactgcaga 350
 aacgagggta gacgaagcag tcattttgac ttaatttctt atggttcata 400
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<212> FRT

<213> Homo sapiens

<400> 273

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| | | 20 | | | | | | 25 | | | | | | 30 |
| Val | Ser | Ala | Trp | Met | Arg | Asp | Tyr | Leu | Asn | Asn | Val | Leu | Thr | Leu |
| | | | 35 | | | | | 40 | | | | | | 45 |
| Thr | Ala | Glu | Thr | Arg | Val | Glu | Glu | Ala | Val | Ile | Leu | Thr | Tyr | Phe |
| | | | 50 | | | | | 55 | | | | | | 60 |
| Pro | Val | Val | His | Pro | Val | Met | Ile | Ala | Val | Cys | Cys | Phe | Leu | Ile |
| | | | 65 | | | | | 70 | | | | | | 75 |
| Ile | Val | Gly | Met | Leu | Gly | Tyr | Cys | Gly | Thr | Val | Lys | Arg | Asn | Leu |
| | | 80 | | | | | | 85 | | | | | | 90 |
| Leu | Leu | Leu | Ala | Trp | Tyr | Phe | Gly | Ser | Leu | Leu | Val | Ile | Phe | Cys |
| | | | 95 | | | | | 100 | | | | | | 105 |
| Val | Glu | Leu | Ala | Cys | Gly | Val | Trp | Thr | Tyr | Glu | Gln | Glu | Leu | Met |
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| Val | Pro | Val | Gln | Trp | Ser | Asp | Met | Val | Thr | Leu | Lys | Ala | Arg | Met |
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| Thr | Asn | Tyr | Gly | Leu | Pro | Arg | Tyr | Arg | Trp | Leu | Thr | His | Ala | Trp |
| | | | 140 | | | | | 145 | | | | | | 150 |
| Asn | Phe | Phe | Gln | Arg | Glu | Ile | Lys | Cys | Cys | Gly | Val | Val | Tyr | Phe |
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| Thr | Asp | Trp | Leu | Glu | Met | Thr | Glu | Met | Asp | Trp | Pro | Pro | Asp | Ser |

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| Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe | | |
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| Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu | | |
| 230 | 235 | 240 |
| Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro | | |
| 245 | 250 | 255 |
| Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His | | |
| 260 | 265 | 270 |
| Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg | | |
| 275 | 280 | 285 |
| Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe | | |
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<213> Homo sapiens

<400> L74

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0111 431

0112 PFT

0113 Homo sapiens

0400 275

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Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
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His Cys Val Lys Ser Phe Pro Gln Gly Pro Ala Val Ala Val Arg
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Phe
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Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
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Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
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Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
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Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
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Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
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Tyr Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
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| 11. Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr | 290 | 295 | 300 |
| Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro | 305 | 310 | 315 |
| Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn | 320 | 325 | 330 |
| Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val | 335 | 340 | 345 |
| 11. Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu | 350 | 355 | 360 |
| Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val | 365 | 370 | 375 |
| Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser | 380 | 385 | 390 |
| Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys | 395 | 400 | 405 |
| Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr | 410 | 415 | 420 |
| Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu | 425 | 430 | |

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 (211): DNA
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 212> FRT
 213> Hinc sapiens
 214> 271

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| Met | Ala | Leu | Pro | Ala | Leu | Gly | Leu | Asp | Pro | Trp | Ser | Leu | Leu | Gly | 15 |
| Leu | Phe | Leu | Phe | Gln | Leu | Leu | Gln | Leu | Leu | Pro | Thr | Thr | Thr | | 20 |
| Ala | Gly | Gly | Gly | Gly | Gln | Gly | Pro | Met | Pro | Arg | Val | Arg | Tyr | Tyr | 35 |
| Ala | Gly | Asp | Glu | Arg | Arg | Ala | Leu | Ser | Phe | Phe | His | Gln | Lys | Gly | 50 |
| Leu | Gln | Asp | Phe | Asp | Thr | Leu | Leu | Leu | Ser | Gly | Asp | Gly | Asn | Thr | 65 |
| Leu | Tyr | Val | Gly | Ala | Arg | Glu | Ala | Ile | Leu | Ala | Leu | Asp | Ile | Gln | 80 |
| Asp | Pro | Gly | Val | Pro | Arg | Leu | Lys | Asn | Met | Ile | Pro | Trp | Pro | Ala | 95 |
| Ser | Asp | Arg | Lys | Lys | Ser | Glu | Cys | Ala | Phe | Lys | Lys | Lys | Ser | Asn | 110 |
| Glu | Thr | Gln | Cys | Phe | Asn | Phe | Ile | Arg | Val | Leu | Val | Ser | Tyr | Asn | 125 |
| Val | Thr | His | Leu | Tyr | Thr | Cys | Gly | Thr | Phe | Ala | Phe | Ser | Pro | Ala | 140 |
| Cys | Thr | Phe | Ile | Gln | Leu | Gln | Asp | Ser | Tyr | Leu | Leu | Pro | Ile | Ser | 155 |
| Glu | Asp | Lys | Val | Met | Glu | Gly | Lys | Gly | Gln | Ser | Pro | Phe | Asp | Pro | 170 |
| Ala | His | Lys | His | Thr | Ala | Val | Leu | Val | Asp | Gly | Met | Leu | Tyr | Ser | 185 |
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| Thr | Leu | Gly | Ser | Gln | Pro | Val | Leu | Lys | Thr | Asp | Asn | Phe | Leu | Arg | 215 |
| Trp | Leu | His | His | Asp | Ala | Ser | Phe | Val | Ala | Ala | Ile | Pro | Ser | Thr | 230 |
| Gln | Val | Val | Tyr | Phe | Phe | Phe | Glu | Glu | Thr | Ala | Ser | Glu | Phe | Asp | 245 |
| Phe | Phe | Glu | Arg | Leu | His | Thr | Ser | Arg | Val | Ala | Arg | Val | Cys | Lys | 260 |
| Asn | Arg | Val | Gly | Gly | Glu | Lys | Leu | Leu | Gln | Lys | Lys | Trp | Thr | Thr | 275 |
| Phe | Leu | Lys | Ala | Gln | Leu | Leu | Cys | Thr | Gln | Pro | Gly | Gln | Leu | Pro | |

| | | | | | |
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| Thr Ala Pro His | Ile Tyr Ala Val | Ile Thr Ser | Gln Trp Gln | Val | 320 |
| Gly Gly Thr Arg | Ser Ser Ala Val | Cys Ala Phe | Ser Leu Leu | Asp | 335 |
| Ile Glu Arg Val | Phe Lys Gly Lys Tyr | Lys Glu Leu | Asn Lys | Glu | 350 |
| Thr Ser Arg Trp | Thr Thr Tyr Arg | Gly Pro Glu | Thr Asn Pro | Arg | 365 |
| Pro Gly Ser Cys | Ser Val Gly Pro | Ser Ser Asp | Lys Ala Leu | Thr | 380 |
| Phe Met Lys Asp | His Phe Leu Met | Asp Glu Gln | Val Val Gly | Thr | 395 |
| Pro Leu Leu Val | Lys Ser Gly Val | Glu Tyr Thr | Arg Leu Ala | Val | 410 |
| Glu Thr Ala Gln | Gly Leu Asp Gly | His Ser His | Leu Val Met | Tyr | 425 |
| Leu Gly Thr Thr | Thr Gly Ser Leu | His Lys Ala | Val Val Ser | Gly | 440 |
| Asp Ser Ser Ala | His Leu Val Glu | Glu Ile Gln | Leu Phe Pro | Asp | 455 |
| Pro Glu Pro Val | Arg Asn Leu Gln | Leu Ala Pro | Thr Gln Gly | Ala | 470 |
| Val Phe Val Gly | Phe Ser Gly Gly | Val Trp Arg | Val Pro Arg | Ala | 485 |
| Asn Cys Ser Val | Tyr Glu Ser Cys | Val Asp Cys | Val Leu Ala | Arg | 500 |
| Asp Pro His Cys | Ala Trp Asp Pro | Glu Ser Arg | Thr Cys Cys | Leu | 515 |
| Leu Ser Ala Pro | Asn Leu Asn Ser | Trp Lys Gln | Asp Met Glu | Arg | 530 |
| Gly Asn Pro Glu | Trp Ala Cys Ala | Ser Gly Pro | Met Ser Arg | Ser | 545 |
| Leu Arg Pro Gln | Ser Arg Pro Gln | Ile Ile Lys | Glu Val Leu | Ala | 560 |
| Val Phe Asn Ser | Ile Leu His Leu | Pro Cys Pro | His Leu Ser | Ala | 575 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Ala | Ser | Tyr | Tyr | Tyr | Ser | His | Gly | Pro | Ala | Ala | Val | Ile | Gln | |
| | | | | | | | | | 620 | | | | | 610 | |
| Ala | Ser | Ser | Thr | Val | Tyr | Asn | Gly | Ser | Leu | Leu | Leu | Ile | Val | Gln | |
| | | | | | | | | | 610 | | | | | 615 | |
| Asp | Gly | Val | Gly | Gly | Leu | Tyr | Gln | Cys | Trp | Ala | Thr | Glu | Asn | Gly | |
| | | | | | | | | | 625 | | | | | 630 | |
| Phe | Ser | Tyr | Pro | Val | Ile | Ser | Tyr | Trp | Val | Asp | Ser | Gln | Asp | Gln | |
| | | | | | | | | | 640 | | | | | 645 | |
| Thr | Leu | Ala | Leu | Asp | Pro | Glu | Leu | Ala | Gly | Ile | Pro | Arg | Glu | His | |
| | | | | | | | | | 655 | | | | | 660 | |
| Val | Lys | Val | Pro | Leu | Thr | Arg | Val | Ser | Gly | Gly | Ala | Ala | Leu | Ala | |
| | | | | | | | | | 670 | | | | | 675 | |
| Ala | Gln | Gln | Ser | Tyr | Trp | Pro | His | Phe | Val | Thr | Val | Thr | Val | Leu | |
| | | | | | | | | | 685 | | | | | 690 | |
| Phe | Ala | Leu | Val | Leu | Ser | Gly | Ala | Leu | Ile | Ile | Leu | Val | Ala | Ser | |
| | | | | | | | | | 700 | | | | | 705 | |
| Pro | Leu | Arg | Ala | Leu | Arg | Ala | Arg | Gly | Lys | Val | Gln | Gly | Cys | Glu | |
| | | | | | | | | | 715 | | | | | 720 | |
| Thr | Leu | Arg | Pro | Gly | Glu | Lys | Ala | Pro | Leu | Ser | Arg | Glu | Gln | His | |
| | | | | | | | | | 730 | | | | | 735 | |
| Leu | Gln | Ser | Pro | Lys | Glu | Cys | Arg | Thr | Ser | Ala | Ser | Asp | Val | Asp | |
| | | | | | | | | | 745 | | | | | 750 | |
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<240> 178

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<210> 179

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0413 Artificial

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0421 Artificial Sequence
0422 1-45
0423 Synthetic Construct.

0490 280
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0490 281
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0492 DNA
0493 Homo sapiens

0490 281
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*2107 282
 *2111 313
 *2112 187
 *2130 Homo sapiens

*4008 282

Met Ala Gly Gln Arg Val Leu Leu Leu Val Gly Phe Leu Leu Pro
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Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr
 20 25 30

Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
 35 40 45

Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
 50 55 60

Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
 65 70

Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
 75 80 85 90

Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
 95 100 105

Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
 110 115 120

Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
 125 130 135

Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
 140 145 150

Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile
 155 160 165

Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro
 170 175 180

Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met
 185 190 195

Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe
 200 205 210

Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile
 215 220 225

Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu
 230 235 240

Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe
 245 250 255

Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly

| | | |
|---|-----|-----|
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| Leu Met Glu Lys Pro Ile Lys Pro Val Pro Gln Asp Leu Glu Asn | | |
| 275 | 280 | 285 |
| Phe Ile Ala Lys Phe Gly Asp Ser Gly Phe Val Leu Val Thr Leu | | |
| 290 | 295 | 300 |
| Gly Ser Met Val Asn Thr Cys Gln Asn Pro Glu Ile Phe Lys Glu | | |
| 305 | 310 | 315 |
| Met Asn Asn Ala Phe Ala His Leu Pro Gln Gly Val Ile Trp Lys | | |
| 320 | 325 | 330 |
| Cys Gln Cys Ser His Trp Pro Lys Asp Val His Leu Ala Ala Asn | | |
| 335 | 340 | 345 |
| Val Lys Ile Val Asp Trp Leu Pro Gln Ser Asp Leu Leu Ala His | | |
| 350 | 355 | 360 |
| Pro Ser Ile Arg Leu Phe Val Thr His Gly Gly Gln Asn Ser Ile | | |
| 365 | 370 | 375 |
| Met Glu Ala Ile Gln His Gly Val Pro Met Val Gly Ile Pro Leu | | |
| 380 | 385 | 390 |
| Phe Gly Asp Gln Pro Glu Asn Met Val Arg Val Glu Ala Lys Lys | | |
| 395 | 400 | 405 |
| Phe Gly Val Ser His Gln Leu Lys Lys Leu Lys Ala Glu Thr Leu | | |
| 410 | 415 | 420 |
| Ala Leu Lys Met Lys Gln Ile Met Glu Asp Lys Arg Tyr Lys Ser | | |
| 425 | 430 | 435 |
| Ala Ala Val Ala Ala Ser Val Ile Leu Arg Ser His Pro Leu Ser | | |
| 440 | 445 | 450 |
| Pro Thr Gln Arg Leu Val Gly Trp Ile Asp His Val Leu Gln Thr | | |
| 455 | 460 | 465 |
| Gly Gly Ala Thr His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp | | |
| 470 | 475 | 480 |
| His Glu Gln Tyr Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu | | |
| 485 | 490 | 495 |
| Thr Leu Gly Thr Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala | | |
| 500 | 505 | 510 |
| Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr | | |
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210-283
 211-24
 212-INA
 213-Artificial

4200

4210 Artificial Sequence

4220 1-24

4230 Synthetic construct.

4300 283

tggttttgt cactatccc aagg 24

4310 284

4320 24

4330 RNA

4340 Artificial

4400

4410 Artificial Sequence

4420 1-24

4430 Synthetic construct.

4500 284

t tgg ttggt ctccaaagag aggg 24

4610 285

4620 45

4630 DNA

4640 Artificial

4700

4710 Artificial Sequence

4720 1-45

4730 Synthetic construct.

4800 285

cttgaagatg tccacctggc tgcaaatgtg aaaattgtgg actga 45

4910 286

4920 340

4930 DNA

4940 Homo sapiens

5000 286

tggtgtgttga tttgtgggg attttgaaga gaggaggaat aggacaaagg 50

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cccgtcacac acacaaacca tgtttctccat ccccccaggt ccagccctca 150

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2100 287
 2110 205
 2120 PRT
 2130 Homo sapiens

4000 287
 Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser
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 Pro Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly
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 Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys
 35 40 45
 Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly
 50 55 60
 Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala
 65 70 75
 Ala Val Arg Ser His His His Glu Pro Ala Gly Glu Thr Gly Arg
 80 85 90
 Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val Asn Glu
 95 100 105
 Gly Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val
 110 115 120
 Arg Gly Val Tyr Ser Phe Arg Phe His Val Val Lys Val Tyr Asn
 125 130 135
 Arg Gln Thr Val Gln Val Ser Leu Met Leu Asn Thr Trp Pro Val
 140 145 150
 Ile Ser Ala Phe Ala Asn Asp Pro Asp Val Thr Arg Glu Ala Ala
 155 160 165
 Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser

170

175

180

Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser
185 190 195

Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu
200 205

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<223> Synthetic construct.

<400> 188
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<223> Synthetic construct.

<400> 189
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<210> 190
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<223> Synthetic construct.

<400> 190
ctgtgtact gcccttgga cctggggacc gagtgtctct gc 42

<210> 191
<211> 1570
<212> DNA
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ttcacacaggc gacatgactg aacacacattc aacacatgagc aacacacatcc 200
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110> 222
 111> 223
 112> 224
 113> Homo sapiens

400> 292

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Leu | Ile | Ala | Ala | Tyr | Ser | Gly | Val | Leu | Arg | Gly | Glu |
| 1 | | | | 1 | | | | | 10 | | | | | 15 |
| Arg | Gln | Ala | Glu | Ala | Asp | Arg | Ser | Gln | Arg | Ser | His | Gly | Gly | Pro |
| | | | 20 | | | | | | 25 | | | | | 30 |
| Ala | Leu | Ser | Arg | Gln | Gly | Ser | Gly | Arg | Trp | Gly | Thr | Gly | Ser | Ser |
| | | | 35 | | | | | | 40 | | | | | 45 |
| Ile | Leu | Ser | Ala | Leu | Gln | Asp | Leu | Phe | Ser | Val | Thr | Trp | Leu | Asn |
| | | | 50 | | | | | | 55 | | | | | 60 |
| Arg | Ser | Lys | Val | Gln | Lys | Gln | Leu | Gln | Val | Ile | Ser | Val | Leu | Gln |
| | | | 65 | | | | | | 70 | | | | | 75 |
| Trp | Val | Leu | Ser | Phe | Leu | Val | Leu | Gly | Val | Ala | Cys | Ser | Ala | Ile |
| | | | 80 | | | | | | 85 | | | | | 90 |
| Leu | Met | Tyr | Ile | Phe | Cys | Thr | Asp | Cys | Trp | Leu | Ile | Ala | Val | Leu |
| | | | 95 | | | | | | 100 | | | | | 105 |
| Tyr | Phe | Thr | Trp | Leu | Val | Phe | Asp | Trp | Asn | Thr | Pro | Lys | Lys | Gly |
| | | | 110 | | | | | | 115 | | | | | 120 |
| Gly | Arg | Arg | Ser | Gln | Trp | Val | Arg | Asn | Trp | Ala | Val | Trp | Arg | Tyr |
| | | | 125 | | | | | | 130 | | | | | 135 |
| Phe | Arg | Asp | Tyr | Phe | Pro | Ile | Gln | Leu | Val | Lys | Thr | His | Asn | Leu |
| | | | 140 | | | | | | 145 | | | | | 150 |
| Leu | Thr | Thr | Arg | Asn | Tyr | Ile | Phe | Gly | Tyr | His | Pro | His | Gly | Ile |
| | | | 155 | | | | | | 160 | | | | | 165 |
| Met | Gly | Leu | Gly | Ala | Phe | Cys | Asn | Phe | Ser | Thr | Glu | Ala | Thr | Gln |
| | | | 170 | | | | | | 175 | | | | | 180 |
| Val | Ser | Lys | Lys | Phe | Pro | Gly | Ile | Arg | Pro | Tyr | Leu | Ala | Thr | Leu |
| | | | 185 | | | | | | 190 | | | | | 195 |
| Ala | Gly | Asn | Phe | Arg | Met | Pro | Val | Leu | Arg | Glu | Tyr | Leu | Met | Ser |
| | | | 200 | | | | | | 205 | | | | | 210 |
| Gly | Gly | Ile | Cys | Pro | Val | Ser | Arg | Asp | Thr | Ile | Asp | Tyr | Leu | Leu |
| | | | 215 | | | | | | 220 | | | | | 225 |
| Ser | Lys | Asn | Gly | Ser | Gly | Asn | Ala | Ile | Ile | Ile | Val | Val | Gly | Gly |
| | | | 230 | | | | | | 235 | | | | | 240 |
| Ala | Ala | Glu | Ser | Leu | Ser | Ser | Met | Pro | Gly | Lys | Asn | Ala | Val | Thr |
| | | | 245 | | | | | | 250 | | | | | 255 |
| Leu | Arg | Asp | Arg | Lys | Gly | Phe | Val | Lys | Leu | Ala | Leu | Arg | His | Gly |

| | | |
|---|-----|-----|
| 260 | 265 | 270 |
| Ala Arg Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr | | |
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| Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln | | |
| 290 | 295 | 300 |
| Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His | | |
| 305 | 310 | 315 |
| Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr | | |
| 320 | 325 | 330 |
| Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro | | |
| 335 | 340 | 345 |
| Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr | | |
| 350 | 355 | 360 |
| Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr | | |
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| Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn | | |
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 <223> Synthetic construct.

<200> 294
 gccacagaca cccatgacac ttcc 24

<210> 295
 <211> 25
 <212> DNA
 <213> Artificial

<220>

<210 Artificial Sequence
 <211 1-50
 <213 Synthetic construct.

<400 295
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<210 296
 <211 2060
 <212 tNA
 <213 Homo sapiens

<400 296
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 <213> Homo sapiens

<400> 297
 Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
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 Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
 20 25 30
 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
 35 40 45
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
 50 55 60
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
 65 70 75
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala
 80 85 90
 Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly
 95 100 105
 Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val
 110 115 120
 Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr
 125 130 135
 Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu
 140 145 150
 Asp Asp Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
 155 160 165

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Phe | Leu | Tyr | Met | Trp | Phe | Leu | Ile | Tyr | Cys | Gln | Gly | Thr | Arg | Phe | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| Thr | Gln | Thr | Lys | His | Arg | Val | Ser | Met | Gln | Val | Ala | Ala | Ala | Lys | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Gly | Leu | Phe | Val | Leu | Lys | Tyr | His | Leu | Leu | Pro | Arg | Thr | Lys | Gly | |
| | | | | 200 | | | | | 205 | | | | | 210 | |
| Ile | Thr | Thr | Ala | Val | Lys | Cys | Leu | Arg | Gly | Thr | Val | Ala | Ala | Val | |
| | | | | 215 | | | | | 220 | | | | | 225 | |
| Tyr | Asp | Val | Thr | Leu | Asn | Phe | Arg | Gly | Asn | Lys | Asn | Pro | Ser | Leu | |
| | | | | 230 | | | | | 235 | | | | | 240 | |
| Leu | Gly | Ile | Leu | Tyr | Gly | Lys | Lys | Tyr | Glu | Ala | Asp | Met | Cys | Val | |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Arg | Arg | Phe | Pro | Leu | Glu | Asp | Ile | Pro | Leu | Asp | Glu | Lys | Glu | Ala | |
| | | | | 260 | | | | | 265 | | | | | 270 | |
| Ala | Gln | Trp | Leu | His | Lys | Leu | Tyr | Gln | Glu | Lys | Asp | Ala | Leu | Gln | |
| | | | | 275 | | | | | 280 | | | | | 285 | |
| Glu | Ile | Tyr | Asn | Gln | Lys | Gly | Met | Phe | Pro | Gly | Glu | Gln | Phe | Lys | |
| | | | | 290 | | | | | 295 | | | | | 300 | |
| Pro | Ala | Arg | Arg | Pro | Trp | Thr | Leu | Leu | Asn | Phe | Leu | Ser | Trp | Ala | |
| | | | | 305 | | | | | 310 | | | | | 315 | |
| Thr | Ile | Leu | Leu | Ser | Pro | Leu | Phe | Ser | Phe | Val | Leu | Gly | Val | Phe | |
| | | | | 320 | | | | | 325 | | | | | 330 | |
| Ala | Ser | Gly | Ser | Pro | Leu | Leu | Ile | Leu | Thr | Phe | Leu | Gly | Phe | Val | |
| | | | | 335 | | | | | 340 | | | | | 345 | |
| Gly | Ala | Ala | Ser | Phe | Gly | Val | Arg | Arg | Leu | Ile | Gly | Glu | Ser | Leu | |
| | | | | 350 | | | | | 355 | | | | | 360 | |
| Glu | Pro | Gly | Arg | Trp | Arg | Leu | Gln | | | | | | | | |
| | | | | 365 | | | | | | | | | | | |

<310> 298

<311> 24

<312> DNA

<313> Artificial

1362

221 Artificial Sequence

222 1-24

223 Synthetic construct.

<400> 298

cttctctctgt aggtgggaca tctg 24

<210> 136

<211> 21

<212> DNA

<11> Artificial

<117>

<111> Artificial Sequence

<112> 1-51

<123> Synthetic construct.

<400> 200

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<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggttct cgtataaaga gagctgctct acgtgccct cctcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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tgttttagca ctggggcaat tottgcttat ttctttggta ggaaaggggc 150

tcagtttgtt ttgtgggggt ggtg-gcagc aggcgggctt acgcctgata 200

cggccctggg ttagaagggg aggggaagata aacttttata caaatgggga 250

tagctggggt ctgaqacctg ctctctcagt aaaattcctg ggatctgcct 300

atacctcttt ttctctaacc tggcataccc tgcttaagc ctctcagggc 350

ttctctctgt tottaggata aaagtattta gagctacaag agccctcatg 400

ctctgcccc tgcctccctg gccagcttca ttgtacatgt ggtgttctct 450

tgtcttctt gtaatgtggt atgcatggtt gtctttgcac aagctttctc 500

tcttttctgt gacactgttc cctgacccc ccatactctt cctacttaat 550

atgtatctat ctgtgactt tcaattctaa catcattttc tccagggata 600

ctgggtttaa agaatctcat ttgttttaat gctctcataa gaccacttgt 650

ttctttttaa aggtattat cactctctta tatctctatg tgccttttaa 700

ttctatggtt tctctctctt tctctctctt tctctctctt tctctctctt 750

· 211 = 5'3'
 · 211 = 1000
 · 212 = DNA
 · 213 = H. m. sapiens

· 400 = 300

ggttggaata gaaatctatg tcccaaatga tccacccccc tccagctccc 50
 aaggtgctgt gattatatt gtaagccccc gtgtcttccc tctaaacaa 100
 tttttcagca actaataaag cccacaggagt tgaactgcta gattctgac 150
 tatactgtga tggtaattga tctactctt acctacatta aatctgttt 200
 ttattctct tgaactaga ctttaccttc ctaaacada ggtctgtca 250
 ctgtgctctt ggcacaaaac tgaacttccc ttgggaaga gaacagagg 300
 ttctacccc accgtccctt ccaagccggg gacagcccca ccttctggc 350
 ctctcgttgg agcagtgccc tcccaactg tctcagctct gaaggcactg 400
 actcgggcag tccaggtagc tgaagccttt ggtagctggc gctttcaagg 450
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 agcatatct cccactgccc agcatcaga cttgtcttat tcaatcactg 550
 ccttgggggc aggaaggccc gtggacactt gtcagagagc agtgggtcag 600
 acatcargct gccgcgccat ctaacctttt catgtcttgc acatcactg 650
 atccatgggc taatctgaac tctgtcccaa ggaacccaga gcttgagtga 700
 actgtgcttc agaccagaa ggggtctgct taccacact ggtttatgtg 750
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 gtggcagggc aggaacttgt ccaaaattat ggttcagaaa agatggagat 850
 gttgggttat cacaagccat cagctctctt gcattcagtg gacatgtggg 900
 gaaagggctg ccgatggccc atgacacact cgggactcac ctctggggcc 950
 atcagacagc cgtttccgcc ccaatccagc taccagctgc tgaaggcaca 1000
 ctacaggccc atgtctctat cagccagcca gaagccaaaa tctgcgata 1050
 ccagccaggc cagagcctct ccaaggagc aagcaaatg accatttctc 1100
 ctccctctct tccctctgag agccctctt atctccctac taaagccacc 1150
 ccaaaatct aattatatt gttatatt tcaatgttgc ccaagcaat 1200
 tcaaaatct tcaatctat tcaatctat tcaatctat tcaatctat 1250

| | | | |
|---|-----|-----|-----|
| Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu | 65 | 70 | 75 |
| Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Gln Gln | 80 | 85 | 90 |
| Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys | 95 | 100 | 105 |
| Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu | 110 | 115 | 120 |
| Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val | 125 | 130 | 135 |
| Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala | 140 | 145 | 150 |
| Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu | 155 | 160 | 165 |
| Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp | 170 | 175 | 180 |
| Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr | 185 | 190 | 195 |
| Glu Arg Cys Leu Glu Leu Leu Arg Pro Gly Gly Ile Leu Ala Val | 200 | 205 | 210 |
| Leu Arg Val Leu Trp Arg Gly Lys Val Leu Glu Pro Pro Lys Gly | 215 | 220 | 225 |
| Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg | 230 | 235 | 240 |
| Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly | 245 | 250 | 255 |
| Leu Thr Leu Ala Phe Lys Ile | 260 | | |

0010 - 307

0011 - 2272

0012 - DNA

0013 - Homo sapiens

0400 - 307

ccgcgcgcgc agcgcgtacc gccgctgcag ccgctttccg cggcctgggc 50

ctctcgccgt cagcatgccca cagccttcca agcccgggga ctgggtgttc 100

gctaagatga agggctaccc tcactggcct gccaggtatg accacatccc 150

ggatggcgcc gtgaagcccc caccacacaa gtacccatc tttttctttg 200

gacacacaca cacagccttc ctgggaccca agaaccttt cccctatgac 250

aatgtttaaag aatattatgg gaaggtttaa aatatttaaag gattttatda 300
 aggtgtttgtt gattttatda aatatttaa aggtttatda aggtttatda 350
 aggtttatda gattttatda aggtttatda aggtttatda aggtttatda 400
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 aggtttatda gattttatda aggtttatda aggtttatda aggtttatda 500
 aggtttatda gattttatda aggtttatda aggtttatda aggtttatda 550
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 aggtttatda gattttatda aggtttatda aggtttatda aggtttatda 650
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 aggggtttt tggagattt tttttttt tttttttt tttttttt 1800
 tttttttt tttttttt tttttttt tttttttt tttttttt 1850
 tttttttt tttttttt tttttttt tttttttt tttttttt 1900
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 tttttttt tttttttt tttttttt tttttttt tttttttt 2000
 tttttttt tttttttt tttttttt tttttttt tttttttt 2050
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4210- 308
 4211- 671
 4212- PRT
 4213- Homo sapiens

4400- 308
 Met Pro His Ala Phe Lys Pro Gly Asp Leu Val Phe Ala Lys Met
 1 5 10 15
 Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Asp Ile Ala Asp
 20 25 30
 Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe
 35 40 45
 Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
 50 55 60
 Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
 65 70 75
 Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
 80 85 90
 Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala
 95 100 105
 Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
 110 115 120
 Thr Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
 125 130 135
 Ala Ser Asp Arg Met Ala Ser Asp Ser Asp Ser Asp Lys Ser Ser

| | | |
|---|-----|-----|
| 145 | 145 | 14 |
| Asp Asn Ser Gly Leu Lys Arg Lys Thr Pro Ala Leu Lys Met Ser | 155 | 165 |
| Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala | 170 | 180 |
| Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu | 185 | 195 |
| Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala | 200 | 210 |
| Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys | 215 | 225 |
| Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser | 230 | 240 |
| Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser | 245 | 255 |
| Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val | 260 | 270 |
| Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro | 275 | 285 |
| Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser | 290 | 300 |
| Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu | 305 | 315 |
| Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg Glu Leu Glu Ala Arg | 320 | 330 |
| Arg Arg Arg Glu Gln Glu Glu Glu Leu Arg Arg Leu Arg Glu Gln | 335 | 345 |
| Glu Lys Glu Glu Lys Glu Arg Arg Arg Glu Arg Ala Asp Arg Gly | 350 | 360 |
| Glu Ala Glu Arg Gly Ser Gly Gly Ser Ser Gly Asp Glu Leu Arg | 365 | 375 |
| Glu Asp Asp Glu Pro Val Lys Lys Arg Gly Arg Lys Gly Arg Gly | 380 | 390 |
| Arg Gly Pro Pro Ser Ser Ser Asp Ser Glu Pro Glu Ala Glu Leu | 395 | 405 |
| Gln Arg Glu Ala Lys Lys Ser Ala Lys Lys Pro Gln Ser Ser Ser | 410 | 420 |
| Thr Gln Pro Ala Arg Lys Pro Gly Gln Lys Ser Lys Arg Val Arg | 425 | 435 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gln | Gln | Lys | Gln | Gln | Ala | Lys | Pro | Val | Lys | Val | Gln | Arg | Thr | 440 | 441 | 442 |
| Arg | Lys | Arg | Ser | Gln | Gly | Phe | Ser | Met | Asp | Arg | Lys | Val | Glu | Lys | 450 | 451 | 452 |
| Lys | Lys | Glu | Pro | Ser | Val | Glu | Glu | Lys | Leu | Gln | Lys | Leu | His | Ser | 460 | 461 | 462 |
| Gln | Ile | Lys | Phe | Ala | Leu | Lys | Val | Asp | Ser | Pro | Asp | Val | Lys | Arg | 470 | 471 | 472 |
| Cys | Leu | Asn | Ala | Leu | Glu | Glu | Leu | Gly | Thr | Leu | Gln | Val | Thr | Ser | 480 | 481 | 482 |
| Gln | Ile | Leu | Gln | Lys | Asn | Thr | Asp | Val | Val | Ala | Thr | Leu | Lys | Lys | 490 | 491 | 492 |
| Ile | Arg | Arg | Tyr | Lys | Ala | Asn | Lys | Asp | Val | Met | Glu | Lys | Ala | Ala | 500 | 501 | 502 |
| Gln | Val | Tyr | Thr | Arg | Leu | Lys | Ser | Arg | Val | Leu | Gly | Pro | Lys | Ile | 510 | 511 | 512 |
| Gln | Ala | Val | Gln | Lys | Val | Asn | Lys | Ala | Gly | Met | Glu | Lys | Glu | Lys | 520 | 521 | 522 |
| Ala | Glu | Gln | Lys | Leu | Ala | Gly | Glu | Glu | Leu | Ala | Gly | Glu | Glu | Ala | 530 | 531 | 532 |
| Pro | Gln | Gln | Lys | Ala | Glu | Asp | Lys | Pro | Ser | Thr | Asp | Leu | Ser | Ala | 540 | 541 | 542 |
| Pro | Val | Asn | Gly | Glu | Ala | Thr | Ser | Gln | Lys | Gly | Glu | Ser | Ala | Gln | 550 | 551 | 552 |
| Asp | Lys | Glu | His | Glu | Glu | Gly | Arg | Asp | Ser | Glu | Glu | Gly | Pro | Arg | 560 | 561 | 562 |
| Cys | Gly | Ser | Ser | Gln | Asp | Leu | His | Asp | Ser | Val | Arg | Glu | Gly | Pro | 570 | 571 | 572 |
| Asp | Leu | Asp | Arg | Pro | Gly | Ser | Asp | Arg | Gln | Glu | Arg | Glu | Arg | Ala | 580 | 581 | 582 |
| Arg | Gly | Asp | Ser | Glu | Ala | Leu | Asp | Glu | Glu | Ser | | | | | 590 | 591 | 592 |

<210> 309

<210> 3871

<210> DNA

<210> Homo sapiens

<400> 309

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 atattcaagg actatcaat catcttgaa atcaattat ctctgaagca 150
 gcaacaattt taatattggtt ccagagatcg attagttcag ctctccttgc 1700
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 aatttaaga aaagaattcc ttactataa aaacattgac ttctgttttg 2500
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 cccgaattt gatagtgtat aaggtgcttt attcctcga atgtccatta 2800
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 acaatttaag acaattccca ttatgaagc gaaattcttc agtgagccat 2950
 tcaactctag acaatgctat acaatttgg acaatgctat taattcttc 3000

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 tacttaatttt tccccagga ttctctatttt ctagtccagga gtaacagpctt 3100
 acagagagga agtttggtgtt taattatgtt ttttttagag tatatactaa 3150
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 atattttaat aaaacaagga aaacataatg atgtataatg catcttgatg 3250
 ggaaggcatg cagatgggat ttgttagaag acagaaggaa agacagccat 3300
 aaattctygc ttgggggaaa actcatatcc ccattgaaaag gaagaacaat 3350
 cacaaataaa gtgagagtaa tctaatggag ctctttttcac taggggtataa 3400
 gtagtgcaca atttgtaatt catctgttaa aaaaaatcta gattataaca 3450
 aactgctagc aaaatctgag gaaacataaa ttctttctgaa gaatcatagg 3500
 aagagttagac attttattttt aaaccaatga tatttcagta tatattttct 3550
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 agaaaaaaa tatataacac acagagaatt aagaaaaatga catttctggg 3700
 agtgggggat atatatttgt tgaataacag aacgagtgtt aaattttaac 3750
 aacggaaaag gttaaattaa ctcttttgaa tcttcaactca accttttctc 3800
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 ataaataagc ctgctacatg t 3871

<310> 310
 <311> 777
 <312> FRT
 <313> Homo sapiens

<400> 310
 Met Asn Ala Asn Lys Asp Glu Arg Leu Lys Ala Arg Ser Gln Asp
 1 5 10 15
 Phe His Leu Phe Pro Ala Ieu Met Met Leu Ser Met Thr Met Leu
 20 25 30
 Phe Ieu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Ieu
 35 40 45
 Lys Ieu Thr Tyr Lys Asp Ieu Ieu Ieu Ser Asn Ser Cys Ile Ieu
 50 55 60
 Phe Ieu Gly Ser Ser Glu Gly Ieu Asp Phe Gln Thr Ieu Ieu Ieu
 65 70 75
 Asp Glu Gly Arg Gly Arg Ieu Ieu Ieu Gly Ala Lys Asp His Ile

80

85

90

Phe Leu Leu Ser Leu Val Asp Leu Asn Lys Asn Phe Lys Lys Ile
105 100 105

Tyr Trp Pro Ala Ala Lys Glu Arg Val Glu Leu Cys Lys Leu Ala
110 115 120

Gly Lys Asp Ala Asn Thr Glu Cys Ala Asn Phe Ile Arg Val Leu
125 130 135

Gln Pro Tyr Asn Lys Thr His Ile Tyr Val Cys Gly Thr Gly Ala
140 145 150

Phe His Pro Ile Cys Gly Tyr Ile Asp Leu Gly Val Tyr Lys Glu
155 160 165

Asp Ile Ile Phe Lys Leu Asp Thr His Asn Leu Glu Ser Gly Arg
170 175 180

Leu Lys Cys Pro Phe Asp Pro Gln Gln Pro Phe Ala Ser Val Met
185 190 195

Thr Asp Glu Tyr Leu Tyr Ser Gly Thr Ala Ser Asp Phe Leu Gly
200 205 210

Lys Asp Thr Ala Phe Thr Arg Ser Leu Gly Pro Thr His Asp His
215 220 225

His Tyr Ile Arg Thr Asp Ile Ser Glu His Tyr Trp Leu Asn Tyr
230 235 240

Ala Lys Phe Ile Gly Thr Phe Phe Ile Pro Asp Thr Tyr Asn Pro
245 250 255

Asp Asp Asp Lys Ile Tyr Phe Phe Phe Arg Glu Ser Ser Gln Glu
260 265 270

Gly Ser Thr Ser Asp Lys Thr Ile Leu Ser Arg Val Gly Arg Val
275 280 285

Cys Lys Asn Asp Val Gly Gly Gln Arg Ser Leu Ile Asn Lys Trp
290 295 300

Thr Thr Phe Leu Lys Ala Arg Leu Ile Cys Ser Ile Pro Gly Ser
305 310 315

Asp Gly Ala Asp Thr Tyr Phe Asp Glu Leu Gln Asp Ile Tyr Leu
320 325 330

Leu Pro Thr Arg Asp Glu Arg Asn Pro Val Val Tyr Gly Val Phe
335 340 345

Thr Thr Thr Ser Ser Ile Phe Lys Gly Ser Ala Val Cys Val Tyr
350 355 360

Ser Met Ala Asp Ile Arg Ala Val Phe Asn Gly Pro Tyr Ala His
365 370 375

380

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gln | Ser | Ala | Asp | His | Arg | Trp | Val | Gln | Tyr | Asp | Gly | Arg | Ile | 380 | 385 | 390 |
| Pro | Tyr | Pro | Arg | Pro | Gly | Thr | Cys | Pro | Ser | Lys | Thr | Tyr | Asp | Pro | 395 | 400 | 405 |
| Leu | Ile | Lys | Ser | Thr | Arg | Asp | Phe | Pro | Asp | Asp | Val | Ile | Ser | Phe | 410 | 415 | 420 |
| Ile | Lys | Arg | His | Ser | Val | Met | Tyr | Lys | Ser | Val | Tyr | Pro | Val | Ala | 425 | 430 | 435 |
| Gly | Gly | Pro | Thr | Phe | Lys | Arg | Ile | Asn | Val | Asp | Tyr | Arg | Leu | Thr | 440 | 445 | 450 |
| Gln | Ile | Val | Val | Asp | His | Val | Ile | Ala | Gln | Asp | Gly | Gln | Tyr | Asp | 455 | 460 | 465 |
| Val | Met | Phe | Leu | Gly | Thr | Asp | Ile | Gly | Thr | Val | Leu | Lys | Val | Val | 470 | 475 | 480 |
| Ser | Ile | Ser | Lys | Gln | Lys | Trp | Asn | Met | Gln | Glu | Val | Val | Leu | Gln | 485 | 490 | 495 |
| Glu | Leu | Gln | Ile | Phe | Lys | His | Ser | Ser | Ile | Ile | Leu | Asn | Met | Glu | 500 | 505 | 510 |
| Leu | Ser | Leu | Lys | Gln | Gln | Gln | Leu | Tyr | Ile | Gly | Ser | Arg | Asp | Gly | 515 | 520 | 525 |
| Leu | Val | Gln | Leu | Ser | Leu | His | Arg | Cys | Asp | Thr | Tyr | Gly | Lys | Ala | 530 | 535 | 540 |
| Cys | Ala | Asp | Cys | Cys | Leu | Ala | Arg | Asp | Pro | Tyr | Cys | Ala | Trp | Asp | 545 | 550 | 555 |
| Gly | Asn | Ala | Cys | Ser | Arg | Tyr | Ala | Pro | Thr | Ser | Lys | Arg | Arg | Ala | 560 | 565 | 570 |
| Arg | Arg | Gln | Asp | Val | Lys | Tyr | Gly | Asp | Pro | Ile | Thr | Gln | Cys | Trp | 575 | 580 | 585 |
| Asp | Ile | Glu | Asp | Ser | Ile | Ser | His | Glu | Thr | Ala | Asp | Glu | Lys | Val | 590 | 595 | 600 |
| Ile | Phe | Gly | Ile | Glu | Phe | Asn | Ser | Thr | Phe | Leu | Glu | Cys | Ile | Pro | 605 | 610 | 615 |
| Lys | Ser | Gln | Gln | Ala | Thr | Ile | Lys | Trp | Tyr | Ile | Gln | Arg | Ser | Gly | 620 | 625 | 630 |
| Asp | Glu | His | Arg | Glu | Glu | Leu | Lys | Pro | Asp | Glu | Arg | Ile | Ile | Lys | 635 | 640 | 645 |
| Thr | Glu | Tyr | Gly | Leu | Leu | Ile | Arg | Ser | Leu | Gln | Lys | Lys | Asp | Ser | 650 | 655 | 660 |
| Gly | Met | Tyr | Tyr | Cys | Lys | Ala | Gln | Gln | His | Thr | Phe | Ile | His | Thr | | | |

| 615 | | | | | | | | | | 670 | | | | | 675 | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Ile | Val | Lys | Leu | Ile | Leu | Asn | Val | Ile | Glu | Asn | Glu | Gln | Met | Glu | | | | | |
| | | | | | | | | | 685 | | | | | 690 | | | | | |
| Asn | Thr | Gln | Arg | Ala | Glu | His | Glu | Glu | Gly | Gln | Val | Lys | Asp | Leu | | | | | |
| | | | | | | | | | 700 | | | | | 705 | | | | | |
| Leu | Ala | Glu | Ser | Arg | Leu | Arg | Tyr | Lys | Asp | Tyr | Ile | Gln | Ile | Leu | | | | | |
| | | | | | | | | | 715 | | | | | 720 | | | | | |
| Ser | Ser | Pro | Asn | Phe | Ser | Leu | Asp | Gln | Tyr | Cys | Glu | Gln | Met | Trp | | | | | |
| | | | | | | | | | 730 | | | | | 735 | | | | | |
| His | Arg | Glu | Lys | Arg | Arg | Gln | Arg | Asn | Lys | Gly | Gly | Pro | Lys | Trp | | | | | |
| | | | | | | | | | 745 | | | | | 750 | | | | | |
| Lys | His | Met | Gln | Glu | Met | Lys | Lys | Lys | Arg | Asn | Arg | Arg | His | His | | | | | |
| | | | | | | | | | 760 | | | | | 765 | | | | | |
| Arg | Asp | Leu | Asp | Glu | Leu | Pro | Arg | Ala | Val | Ala | Thr | | | | | | | | |
| | | | | | | | | | 770 | | | | | | | | | | |

<110> 311
 <111> 25
 <112> DNA
 <113> Artificial

<120>
 <21> Artificial Sequence
 <22> 1-25
 <23> Synthetic construct.

<400> 311
 gacgacgccc gtagataaaca agtgg 25

<110> 312
 <111> 24
 <112> DNA
 <113> Artificial

<120>
 <21> Artificial Sequence
 <22> 1-14
 <23> Synthetic construct.

<400> 312
 gattggaacat gtaccacgccc gtgg 24

<110> 313
 <111> 45
 <112> DNA
 <113> Artificial

<120>
 <21> Artificial Sequence
 <22> 1-41
 <23> Synthetic construct.

<210> 314

ggcattctta atttctctaa ttcttggaag tgataggcca gatac 45

<210> 314

<211> 3934

<212> DNA

<213> Homo sapiens

<400> 314

ccctgacctc cctgagccac actgagctgg aagccgcaga ggtcctcctg 50
jagcatgcac acccggggga gcagacaacc tccaggttaa gctggggaga 100
agactgaag ctgtttcttc aggagcctgg tgtattttcc cccacccccc 150
ctcagcagtt ccagccagca gggactgac aggtgtgtgt cctggagtg 200
ggacccagaag gctgtgctgg caagagtggc ctggagaaag aggttcagcg 250
cttgaccagc ccagctgcac gtgactacaa gatccagaac catgggcctc 300
gggtgaggtg ggggggcaca ggtgtcatgt gcacctctct gtctcagcaa 350
gaagagctga gagaggggat cttggagcca ttgaggggtg catggagcta 400
cagaggggag ggaaggttat tttaaggtaa cagtgtggca caatagttaa 450
gagacagtt tttggagcta gacgacata ggtccaaatt ctctctctgt 500
gcttcctagt cctgtagccc caggttaaggg agtgaactaa cctctctgga 550
cttcaatttc ctcactacta aagtagggac aataatagca cccacccat 600
agggaagatt aatgacata atgtatgtga tgcacctagc aaagtaccag 650
tcccatagta agtcatgccc cacagtattt ccccccaccc ctgttctctg 700
ccttcccaac caggtactgc aacgactgga gcagagggcg cagcaggctt 750
cagaggggga ggctccagc atagaacaga ggttacagga agtgcagag 800
agcctccgcc gggcacaggt gagccaggtg aaggggctg ccggctggc 850
cctgctgcag ggggtggt tagatgtgga gctgtggtg aagccagcca 900
tgacccaggc ccaggatgag gtggagcagg agcggcggt cagtgaggt 950
cggtgtctcc agagggacct ctctcccaac gctgaggtat ctgagcttc 1000
tgactttgag gaatgtgagg agacgggaga gctctttgag gagcctgccc 1050
cccagccct ggcacagag gccctccct gccctgcac cgtggtattt 1100
cgctatcagg cagggcgtga ggatgagctg acaatcagg agggtgagta 1150
cctgga gtc atagaggag gatatgctga cgaatgggtc aaggctcgga 1200
ccagacac ccagtaggc ttgtctctt agcgaatct caactcccg 1250

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Phe | Pro | Pro | Thr | Pro | Val | Leu | Cys | Leu | Pro | Asn | Gln | Val | Leu | |
| | | | | 20 | | | | | 35 | | | | | 40 | |
| Gln | Arg | Leu | Glu | Gln | Arg | Arg | Gln | Gln | Ala | Ser | Glu | Arg | Glu | Ala | |
| | | | | 35 | | | | | 40 | | | | | 45 | |
| Pro | Ser | Ile | Glu | Gln | Arg | Leu | Gln | Glu | Val | Arg | Glu | Ser | Ile | Arg | |
| | | | | 50 | | | | | 55 | | | | | 60 | |
| Arg | Ala | Gln | Val | Ser | Gln | Val | Lys | Gly | Ala | Ala | Arg | Leu | Ala | Leu | |
| | | | | 65 | | | | | 70 | | | | | 75 | |
| Leu | Gln | Gly | Ala | Gly | Leu | Asp | Val | Glu | Arg | Trp | Leu | Lys | Pro | Ala | |
| | | | | 80 | | | | | 85 | | | | | 90 | |
| Met | Thr | Gln | Ala | Gln | Asp | Gln | Val | Glu | Gln | Glu | Arg | Arg | Leu | Ser | |
| | | | | 95 | | | | | 100 | | | | | 105 | |
| Glu | Ala | Arg | Leu | Ser | Gln | Arg | Asp | Leu | Ser | Pro | Thr | Ala | Glu | Asp | |
| | | | | 110 | | | | | 115 | | | | | 120 | |
| Ala | Glu | Leu | Ser | Asp | Phe | Glu | Glu | Cys | Glu | Gln | Thr | Gly | Glu | Leu | |
| | | | | 125 | | | | | 130 | | | | | 135 | |
| Phe | Glu | Glu | Pro | Ala | Pro | Gln | Ala | Leu | Ala | Thr | Arg | Ala | Leu | Pro | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Cys | Pro | Ala | His | Val | Val | Phe | Arg | Tyr | Gln | Ala | Gly | Arg | Glu | Asp | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Glu | Leu | Thr | Ile | Thr | Glu | Gly | Glu | Trp | Leu | Glu | Val | Ile | Glu | Gln | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| Gly | Asp | Ala | Asp | Glu | Trp | Val | Lys | Ala | Arg | Asn | Gln | His | Gly | Glu | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Val | Gly | Phe | Val | Pro | Glu | Arg | Tyr | Leu | Asn | Phe | Pro | Asp | Leu | Ser | |
| | | | | 200 | | | | | 205 | | | | | 210 | |
| Leu | Pro | Glu | Ser | Ser | Gln | Asp | Ser | Asp | Asn | Pro | Cys | Gly | Ala | Glu | |
| | | | | 215 | | | | | 220 | | | | | 225 | |
| Pro | Thr | Ala | Phe | Leu | Ala | Gln | Ala | Leu | Tyr | Ser | Tyr | Thr | Gly | Gln | |
| | | | | 230 | | | | | 235 | | | | | 240 | |
| Ser | Ala | Glu | Glu | Leu | Ser | Phe | Pro | Glu | Gly | Ala | Leu | Ile | Arg | Leu | |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Leu | Pro | Arg | Ala | Gln | Asp | Gly | Val | Asp | Asp | Gly | Phe | Trp | Arg | Gly | |
| | | | | 260 | | | | | 265 | | | | | 270 | |
| Glu | Phe | Gly | Gly | Arg | Val | Gly | Val | Phe | Pro | Ser | Leu | Leu | Val | Glu | |
| | | | | 275 | | | | | 280 | | | | | 285 | |
| Gln | Leu | Leu | Gly | Pro | Pro | Gly | Pro | Pro | Glu | Leu | Ser | Asp | Pro | Glu | |
| | | | | 290 | | | | | 295 | | | | | 300 | |
| Gln | Met | Leu | Pro | Ser | Pro | Ser | Pro | Pro | Ser | Phe | Ser | Pro | Pro | Ala | |

| | | | |
|---|-----|-----|-----|
| 312 | 313 | 314 | 315 |
| Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly | | | |
| 323 | 324 | | 330 |
| Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro | | | |
| 335 | 340 | | 345 |
| Arg Leu Arg Pro Met Arg Pro Pro Pro Pro Pro Ala Lys Ala | | | |
| 350 | 355 | | 360 |
| Pro Asp Pro Gly His Pro Asp Pro Leu Thr | | | |
| 365 | 370 | | |

<210> 316

<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

cacaggaggaga accacagaca catatgcacg agagagacag aggaggaaag 50
 agacagagac aaaggacacg cgggaagaagg cagagacagg gcaggcacag 100
 aagcggccca gacagagtcg tacagaggga gaggcacag aagctgcaga 150
 adacacagga agggagagac aaagatccag gaaaggaggg ctacaggaga 200
 gactttggag aagccagacc cctgggcacc tctcacaagg ccaaggacta 250
 agttttctcc atttccttta acggtctctc ggcctctctg aaactttgac 300
 tctgaccttj gcaggagtcc aagccccag gctacajaga ggagctttcc 350
 aaactatagg tctggaggac ttggtgcctt agacggcctc agtccctccc 400
 agctgcagta ccagtgcctt ctcccagaca ggctcgcctc cggggagggg 450
 ctltggcagg gctgcctgt ggggagccca acctgcctc ctgctcccca 500
 ttgtgccgtt ctctgggtg gtgtgggtgc ttctgctact gctggcctct 550
 ctctgcctt cagccgggtt ggcacgccc ctcccgggg aggaggagat 600
 cgtgtttcca gagaagctca acggcagcgt cctgcctggc tggggcgccc 650
 ctgccaggct gttgtgcgcg ttgcaggcct ttggggagac gctgctaact 700
 gagctggagc aggaactcgg tgtgcaggtc gaggggctca cagtgcagta 750
 cctgggcacg ggcctcagc tgcctgggtg agcagagcct ggcacctaac 800
 tgaatggcac cactaatgga gctccggagt cggctggcctc tctgaactgg 850
 cctctctctc cctctctcct cctgttctca tatctggggg ctgaactcca 900
 cctctctctc cctctctcct cctctctcct cctctctcct ggaactctgg 950

$$= \frac{1}{2} \left(\frac{1}{2} + \frac{1}{2} \right) = \frac{1}{2}$$

| | | |
|---|-----|-----|
| 144 | 147 | 151 |
| Gly Val Leu Gln Tyr Arg Gly Ala Gln Leu His Leu Gln Pr | Leu | Leu |
| 155 | 160 | 164 |
| Gln Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile | | |
| 170 | 175 | 180 |
| Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn | | |
| 185 | 190 | 195 |
| Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala | | |
| 200 | 205 | 210 |
| Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Gln Thr Leu Val Val | | |
| 215 | 220 | 225 |
| Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg | | |
| 230 | 235 | 240 |
| Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His | | |
| 245 | 250 | 255 |
| Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val | | |
| 260 | 265 | 270 |
| Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala | | |
| 275 | 280 | 285 |
| Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn | | |
| 290 | 295 | 300 |
| Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu | | |
| 305 | 310 | 315 |
| Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu | | |
| 320 | 325 | 330 |
| Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys | | |
| 335 | 340 | 345 |
| Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala | | |
| 350 | 355 | 360 |
| His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys | | |
| 365 | 370 | 375 |
| Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val | | |
| 380 | 385 | 390 |
| Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser | | |
| 395 | 400 | 405 |
| Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr | | |
| 410 | 415 | 420 |
| Gly His Cys Leu Leu Asp Lys Pro Gln Ala Pro Leu His Leu Pr | | |
| 425 | 430 | 435 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Thr | Ile | Trp | Gly | Lys | Arg | Tyr | Arg | Ala | Asp | Arg | Gln | Tyr | Gln | |
| | | | | 445 | | | | | 445 | | | | | 455 | |
| Leu | Thr | Ile | Gly | Arg | Asp | Ser | Ala | His | Cys | Trp | Gln | Leu | Trp | Pro | |
| | | | | 455 | | | | | 465 | | | | | 465 | |
| Pro | Cys | Ala | Ala | Leu | Trp | Cys | Ser | Gly | His | Leu | Asn | Gly | His | Ala | |
| | | | | 470 | | | | | 475 | | | | | 480 | |
| Met | Cys | Gln | Thr | Lys | His | Ser | Pro | Trp | Ala | Asp | Gly | Thr | Pro | Cys | |
| | | | | 485 | | | | | 490 | | | | | 495 | |
| Gly | Pro | Ala | Gln | Ala | Cys | Met | Gly | Gly | Arg | Cys | Leu | His | Met | Asp | |
| | | | | 500 | | | | | 505 | | | | | 510 | |
| Gln | Leu | Gln | Asp | Phe | Asn | Ile | Pro | Gln | Ala | Gly | Gly | Trp | Gly | Pro | |
| | | | | 515 | | | | | 520 | | | | | 525 | |
| Trp | Gly | Pro | Trp | Gly | Asp | Cys | Ser | Arg | Thr | Cys | Gly | Gly | Gly | Val | |
| | | | | 530 | | | | | 535 | | | | | 540 | |
| Gln | Phe | Ser | Ser | Arg | Asp | Cys | Thr | Arg | Pro | Val | Pro | Arg | Asn | Gly | |
| | | | | 545 | | | | | 550 | | | | | 555 | |
| Gly | Lys | Tyr | Cys | Glu | Gly | Arg | Arg | Thr | Arg | Phe | Arg | Ser | Cys | Asn | |
| | | | | 560 | | | | | 565 | | | | | 570 | |
| Thr | Glu | Asp | Cys | Pro | Thr | Gly | Ser | Ala | Leu | Thr | Phe | Arg | Gln | Glu | |
| | | | | 575 | | | | | 580 | | | | | 585 | |
| Gln | Cys | Ala | Ala | Tyr | Asn | His | Arg | Thr | Asp | Leu | Phe | Lys | Ser | Phe | |
| | | | | 590 | | | | | 595 | | | | | 600 | |
| Pro | Gly | Pro | Met | Asp | Trp | Val | Pro | Arg | Tyr | Thr | Gly | Val | Ala | Pro | |
| | | | | 605 | | | | | 610 | | | | | 615 | |
| Gln | Asp | Gln | Cys | Lys | Leu | Thr | Cys | Gln | Ala | Arg | Ala | Leu | Gly | Tyr | |
| | | | | 620 | | | | | 625 | | | | | 630 | |
| Tyr | Tyr | Val | Leu | Glu | Pro | Arg | Val | Val | Asp | Gly | Thr | Pro | Cys | Ser | |
| | | | | 635 | | | | | 640 | | | | | 645 | |
| Pro | Asp | Ser | Ser | Ser | Val | Cys | Val | Gln | Gly | Arg | Cys | Ile | His | Ala | |
| | | | | 650 | | | | | 655 | | | | | 660 | |
| Gly | Cys | Asp | Arg | Ile | Ile | Gly | Ser | Lys | Lys | Lys | Phe | Asp | Lys | Cys | |
| | | | | 665 | | | | | 670 | | | | | 675 | |
| Met | Val | Cys | Gly | Gly | Asp | Gly | Ser | Gly | Cys | Ser | Lys | Gln | Ser | Gly | |
| | | | | 680 | | | | | 685 | | | | | 690 | |
| Ser | Phe | Arg | Lys | Ile | Arg | Tyr | Gly | Tyr | Asn | Asn | Val | Val | Thr | Ile | |
| | | | | 695 | | | | | 700 | | | | | 705 | |
| Pro | Ala | Gly | Ala | Thr | His | Ile | Leu | Val | Arg | His | Gln | Gly | Asn | Pro | |
| | | | | 715 | | | | | 720 | | | | | 725 | |
| Gly | His | Arg | Ser | Ile | Tyr | Leu | Ala | Leu | Tyr | Leu | Trp | Arg | Gly | Ser | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 725 | | 730 | | 735 | | | | | | | | | |
| Tyr | Ala | Leu | Asn | Gly | Glu | Tyr | Thr | Leu | Met | Pro | Ser | Pro | Thr | Asp |
| | | | | 740 | | | | | 745 | | | | | 750 |
| Val | Val | Leu | Pro | Gly | Ala | Val | Ser | Leu | Arg | Tyr | Ser | Gly | Ala | Thr |
| | | | | 755 | | | | | 760 | | | | | 765 |
| Ala | Ala | Ser | Glu | Thr | Leu | Ser | Gly | His | Gly | Pro | Leu | Ala | Gln | Pro |
| | | | | 770 | | | | | 775 | | | | | 780 |
| Leu | Thr | Leu | Gln | Val | Leu | Val | Ala | Gly | Asn | Pro | Gln | Asp | Thr | Arg |
| | | | | 785 | | | | | 790 | | | | | 795 |
| Leu | Arg | Tyr | Ser | Phe | Phe | Val | Pro | Arg | Pro | Thr | Pro | Ser | Thr | Pro |
| | | | | 800 | | | | | 805 | | | | | 810 |
| Arg | Pro | Thr | Pro | Gln | Asp | Trp | Leu | His | Arg | Arg | Ala | Gln | Ile | Leu |
| | | | | 815 | | | | | 820 | | | | | 825 |
| Gln | Ile | Leu | Arg | Arg | Arg | Pro | Trp | Ala | Gly | Arg | Lys | | | |
| | | | | 830 | | | | | 835 | | | | | |

<110> 318
 <111> 23
 <112> DNA
 <113> Artificial

<120>
 <121> Artificial Sequence
 <122> 1-23
 <123> Synthetic construct.

<100> 318
 ccctgaagct gccagatggc tcc 23

<110> 319
 <111> 24
 <112> DNA
 <113> Artificial

<120>
 <121> Artificial Sequence
 <122> 1-24
 <123> Synthetic construct.

<100> 319
 ctatgccttt ccgtgcagcc agtc 24

<110> 320
 <111> 43
 <112> DNA
 <113> Artificial

<120>
 <121> Artificial Sequence
 <122> 1-43
 <123> Synthetic construct.

<400> 320
ccacagatgt ggtactggtt aacacagtta gttttagata ttt 40

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
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gagagaccat ggcaagaat cctccagaa atttgtgaag ctgtccatt 100
ctaaatgcag aagctttttaa atccagaaa atatgtaaat cacttccat 150
ttgtggactg gtgttttggt tcttggcct aactctaat ctctctttt 200
gggggagcaa gaactttctt cgggaggtac ccaaaaaagt ctatgcatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcggaaat ggcactgatg 350
aaacattgga agtgcacgac tttaaaaag cctacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaac cacttaaaag ttaatttga 450
attttctgaa ccagagagaa aaatagatga gaatgaagaa attaccacaa 500
ctttctttta acagtcagtg atttgggttc cagcagaaa cctatttga 550
aacccagatt ttcttaaaaa tctcaaaatt ctggagattt gtgataaagt 600
gaacatgtat tggatcaatc ccactctaat atcagttctt gacttacaag 650
actttgagga ggaggagaa gatcttcaat tctctgocaa cgaaaaaaaa 700
gggattgaac aaaaagaana gtgggttggt cctcaagtga aagtaagaga 750
gaacgtctac gccagacaaag caagtgagga agaacttcca ataaatgaat 800
atactgaaaa tggaatagaa ttgatccca tgctggatga gagaggttat 850
tgttgtattt actgacgttc aggcacccgc tattgcacgc gctctctga 900
acctttacta ggctactanc catatccata ctgctaccaa ggagacagag 950
tcatctctcg tctcatcaca ccttgaact gctcagttgc cctcatgtg 1000
gggagggtct aataggaggt ttgagctcaa atgcttaaac tgcctggcaac 1050
atataatcaa tgcctgtat tcaatgaatt tctgcctatg agccatctgg 1100
cctctgtac ccactcttc acaattact gttaggttaatt ctctcttca 1150
tcttctaatc aattctcaa ttatccaa aaaaaaaa tttttt 1197
210 322

211 - 312
 212 - FET
 213 - H. sapiens

400 - 322

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Asn | Pro | Pro | Glu | Asn | Cys | Glu | Asp | Cys | His | Ile | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |
| Asn | Ala | Glu | Ala | Phe | Lys | Ser | Lys | Lys | Ile | Cys | Lys | Ser | Leu | Lys |
| | | | | 20 | | | | | 25 | | | | | 30 |
| Ile | Cys | Gly | Leu | Val | Phe | Gly | Ile | Leu | Ala | Leu | Thr | Leu | Ile | Val |
| | | | | 35 | | | | | 40 | | | | | 45 |
| Leu | Phe | Trp | Gly | Ser | Lys | His | Phe | Trp | Pro | Glu | Val | Pro | Lys | Lys |
| | | | | 50 | | | | | 55 | | | | | 60 |
| Ala | Tyr | Asp | Met | Glu | His | Thr | Phe | Tyr | Ser | Asn | Gly | Glu | Lys | Lys |
| | | | | 65 | | | | | 70 | | | | | 75 |
| Lys | Ile | Tyr | Met | Glu | Ile | Asp | Pro | Val | Thr | Arg | Thr | Glu | Ile | Phe |
| | | | | 80 | | | | | 85 | | | | | 90 |
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| | | | | 95 | | | | | 100 | | | | | 105 |
| Lys | Asn | Gly | Tyr | Thr | Gly | Ile | Tyr | Phe | Val | Gly | Leu | Gln | Lys | Cys |
| | | | | 110 | | | | | 115 | | | | | 120 |
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| Glu | Glu | Glu | Ile | Asp | Glu | Asn | Glu | Glu | Ile | Thr | Thr | Thr | Phe | Phe |
| | | | | 140 | | | | | 145 | | | | | 150 |
| Glu | Gln | Ser | Val | Ile | Trp | Val | Pro | Ala | Glu | Lys | Pro | Ile | Glu | Asn |
| | | | | 155 | | | | | 160 | | | | | 165 |
| Arg | Asp | Phe | Leu | Lys | Asn | Ser | Lys | Ile | Leu | Glu | Ile | Cys | Asp | Asn |
| | | | | 170 | | | | | 175 | | | | | 180 |
| Val | Thr | Met | Tyr | Trp | Ile | Asn | Pro | Thr | Leu | Ile | Ser | Val | Ser | Glu |
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| Leu | Gln | Asp | Phe | Glu | Glu | Glu | Gly | Glu | Asp | Leu | His | Phe | Pro | Ala |
| | | | | 200 | | | | | 205 | | | | | 210 |
| Asn | Glu | Lys | Lys | Gly | Ile | Glu | Gln | Asn | Glu | Gln | Trp | Val | Val | Pro |
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| Gln | Val | Lys | Val | Glu | Lys | Thr | Arg | His | Ala | Arg | Gln | Ala | Ser | Glu |
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| Asp | Pro | Met | Leu | Asp | Glu | Arg | Gly | Tyr | Cys | Cys | Ile | Tyr | Cys | Arg |
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Tyr Tyr Phe Tyr Phe Tyr Cys Tyr Gln Gly Gly Ala Val Ile Cys
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Arg Val

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<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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 0211: 239
 0212: PWT
 0213: Homo sapiens

0401: 324

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Thr | Ala | Val | Gln | Leu | Leu | Gly | Phe | Leu | Leu | Ser | Phe |
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| Leu | Gly | Met | Val | Gly | Thr | Leu | Ile | Thr | Thr | Ile | Leu | Pro | His | Trp |
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| Arg | Arg | Thr | Ala | His | Val | Gly | Thr | Asn | Ile | Leu | Thr | Ala | Val | Ser |
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| Tyr | Leu | Lys | Gly | Leu | Trp | Met | Glu | Cys | Val | Trp | His | Ser | Thr | Gly |
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| Ile | Tyr | Gln | Cys | Gln | Ile | Tyr | Arg | Ser | Leu | Leu | Ala | Leu | Pro | Gln |
| | | | | 65 | | | | | 70 | | | | | 75 |
| Asp | Leu | Gln | Ala | Ala | Arg | Ala | Leu | Met | Val | Ile | Ser | Cys | Leu | Leu |
| | | | | 80 | | | | | 85 | | | | | 90 |
| Ser | Gly | Ile | Ala | Cys | Ala | Cys | Ala | Val | Ile | Gly | Met | Lys | Cys | Thr |
| | | | | 95 | | | | | 100 | | | | | 105 |
| Arg | Cys | Ala | Lys | Gly | Thr | Pro | Ala | Lys | Thr | Thr | Phe | Ala | Ile | Leu |
| | | | | 110 | | | | | 115 | | | | | 120 |
| Gly | Gly | Thr | Leu | Phe | Ile | Leu | Ala | Gly | Leu | Leu | Cys | Met | Val | Ala |
| | | | | 125 | | | | | 130 | | | | | 135 |
| Val | Ser | Trp | Thr | Thr | Asn | Asp | Val | Val | Gln | Asn | Phe | Tyr | Asn | Pro |
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| Leu | Leu | Pro | Ser | Gly | Met | Lys | Phe | Glu | Ile | Gly | Gln | Ala | Leu | Tyr |
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| Leu | Gly | Phe | Ile | Ser | Ser | Ser | Leu | Ser | Leu | Ile | Gly | Gly | Thr | Leu |
| | | | | 170 | | | | | 175 | | | | | 180 |
| Leu | Cys | Leu | Ser | Cys | Gln | Asp | Glu | Ala | Pro | Tyr | Arg | Pro | Tyr | Gln |
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| Ala | Pro | Pro | Arg | Ala | Thr | Thr | Thr | Thr | Ala | Asn | Thr | Ala | Pro | Ala |
| | | | | 200 | | | | | 205 | | | | | 210 |
| Tyr | Gln | Pro | Pro | Ala | Ala | Tyr | Lys | Asp | Asn | Arg | Ala | Pro | Ser | Val |
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aagaagatat accatggagg tccccgaca gaggaacgag taacatctta 850
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 <213> Homo sapiens

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 35 40 45
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

| 40 | 65 | 90 |
|-------------------------------------|-------------------------|-----|
| Ala Ile Gly Leu Leu Val Ser Ile Phe | Ala Leu Lys Cys Ile Arg | |
| 95 | 100 | 105 |
| Ile Gly Ser Met Thr Asp Ser Ala Lys | Ala Asn Met Thr Leu Thr | |
| 110 | 115 | 120 |
| Ser Gly Ile Met Phe Ile Val Ser Gly | Leu Cys Ala Ile Ala Gly | |
| 125 | 130 | 135 |
| Val Ser Val Phe Ala Asn Met Leu Val | Thr Asn Phe Trp Met Ser | |
| 140 | 145 | 150 |
| Thr Ala Asn Met Tyr Thr Gly Met Gly | Gly Met Val Gln Thr Val | |
| 155 | 160 | 165 |
| Gln Thr Arg Tyr Thr Phe Gly Ala Ala | Leu Phe Val Gly Trp Val | |
| 170 | 175 | 180 |
| Ala Gly Gly Leu Thr Leu Ile Gly Gly | Val Met Met Cys Ile Ala | |
| 185 | 190 | 195 |
| Cys Arg Gly Leu Ala Pro Glu Glu Thr | Asn Tyr Lys Ala Val Ser | |
| 200 | 205 | 210 |
| Tyr His Ala Ser Gly His Ser Val Ala | Tyr Lys Pro Gly Gly Phe | |
| 215 | 220 | 225 |
| Lys Ala Ser Thr Gly Phe Gly Ser Asn | Thr Lys Asn Lys Lys Ile | |
| 230 | 235 | 240 |
| Tyr Asp Gly Gly Ala Arg Thr Glu Asp | Glu Val Gln Ser Tyr Pro | |
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| Ser Lys His Asp Tyr Val | | |
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| | | | | | | | | | | | | | |
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| Thr | Gly | Lys | Ile | Ser | Pro | Val | Tyr | Pro | Arg | Ser | Gln | Tyr | Val |
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Accepted Manuscript

Manuscript to be reviewed

<210> 335

<211> 220

<212> PRT

<213> Homo sapiens

<400> 350

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20 25 30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
35 40 45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
50 55 60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
80 85 90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
95 100 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
110 115 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
125 130 135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
140 145 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
155 160 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu
170 175 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
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Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
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<211> 1160

<212> DNA

<11> Homo sapiens

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<11> 173

<12> 187

<13> Homo sapiens

<40> 432

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| 20 | 25 | 30 | |
| Ala | Leu | Met | Cys |
| 35 | 40 | 45 | |
| Ile | Gly | Ile | Cys |
| 50 | 55 | 60 | |
| Gln | Arg | Ala | Lys |
| 65 | 70 | 75 | |
| Ile | Leu | Thr | Gly |
| 80 | 85 | 90 | |
| Asn | Ile | Ile | Ile |
| 95 | 100 | 105 | |
| Gln | Lys | Arg | Gln |
| 110 | 115 | 120 | |
| Ala | Ala | Val | Leu |
| 125 | 130 | 135 | |
| Cys | Cys | Asn | Arg |
| 140 | 145 | 150 | |
| Tyr | Arg | Val | Pro |
| 155 | 160 | 165 | |
| Ser | Lys | Thr | Ser |
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 ggaagtatcc agtgggtgsc atccctgccc ccattcacata cctaccagtt 200
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 gaccttgaaa agtaatggaa gatttcagtt tottccagat ggaagttgct 300
 caatttcaca tggacataga gaaaaaggaa tcatattctc atcatcatct 350
 tcatcatccc auctatgac taagtttttt taagttttac tcatgtctctg 400
 ctatcttccc atggttggat tctatcaat ctggaatgaa tggagaaatt 450

111710> 334 cccatgacaa ccgatgctc actgacacac gacgatcttt 500

cttgagagc gtcataaaa gataatctc ccaga (3)

111711> 334

211> 85

212> 18T

213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15

Ile Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

1210> 335

211> 342

212> 1NA

213> Homo sapiens

<400> 335

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ctgctcgccc cccgcgcgca tggctgctc cccgcgcggg cctgctgtcc 100

tgccttgac cggcttggg ctgctctgc tctgtgtg gggccaggt 150

ggcataactg gaaataaact caagctgatg ctcaaaaaa gagaagcacc 200

tgttcgaact aagactaaag tggcgttga tgagaataaa gccaaagaat 250

tcttggcag cctgaagcgc cagaagcggc agctgtggga ccggaactcg 300

ccggaagtgc agcagfggta ccagcagttt ctctacatg gctttgatga 350

acggaaattt gaagatgaca tcaactattg gcttaacada gatcgaaatg 400

gcctgaata ctatccgat tactacaaac gtcactatga tgaagactct 450

gcaatgggtc cccnagccc ctacggttt aggcattggag ccagcgtcaa 500

ctccctgac tactaaact gattgccc acgctctacg agagcgaat 550

acattctt ctctctatc tctaaatcc ctacattact tggctctgca 600

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<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
 1 10 15

Leu Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
 20 25 30

Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
 35 40 45

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Leu | Thr | Pro | Ser | Gln | Pro | Ser | Ala | Ala | Met | Ala | Ala | Thr | Asp | |
| | | | | 11 | | | | | 15 | | | | | 60 | |
| Ser | Met | Arg | Gly | Glu | Ala | Pro | Gly | Ala | Glu | Thr | Pro | Ser | Leu | Arg | |
| | | | | 65 | | | | | 70 | | | | | 75 | |
| His | Arg | Gly | Gln | Ala | Ala | Gln | Pro | Glu | Pro | Ser | Thr | Gly | Phe | Thr | |
| | | | | 80 | | | | | 85 | | | | | 90 | |
| Ala | Thr | Pro | Pro | Ala | Pro | Asp | Ser | Pro | Gln | Glu | Pro | Leu | Val | Leu | |
| | | | | 95 | | | | | 100 | | | | | 105 | |
| Arg | Leu | Lys | Phe | Leu | Asn | Asp | Ser | Glu | Gln | Val | Ala | Arg | Ala | Trp | |
| | | | | 110 | | | | | 115 | | | | | 120 | |
| Pro | His | Asp | Thr | Ile | Gly | Ser | Leu | Lys | Arg | Thr | Gln | Phe | Pro | Gly | |
| | | | | 125 | | | | | 130 | | | | | 135 | |
| Arg | Glu | Gln | Gln | Val | Arg | Leu | Ile | Tyr | Gln | Gly | Gln | Leu | Leu | Gly | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Asp | Asp | Thr | Gln | Thr | Leu | Gly | Ser | Leu | His | Leu | Pro | Pro | Asn | Cys | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Val | Leu | His | Cys | His | Val | Ser | Thr | Arg | Val | Gly | Pro | Pro | Asn | Pro | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| Pro | Cys | Pro | Pro | Gly | Ser | Glu | Pro | Gly | Pro | Ser | Gly | Leu | Glu | Ile | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Gly | Ser | Leu | Leu | Leu | Pro | Leu | Leu | Leu | Leu | Leu | Leu | Leu | Leu | Leu | |
| | | | | 200 | | | | | 205 | | | | | 210 | |
| Trp | Tyr | Cys | Gln | Ile | Gln | Tyr | Arg | Pro | Phe | Phe | Pro | Leu | Thr | Ala | |
| | | | | 215 | | | | | 220 | | | | | 225 | |
| Thr | Leu | Gly | Leu | Ala | Gly | Phe | Thr | Leu | Leu | Leu | Ser | Leu | Leu | Ala | |
| | | | | 230 | | | | | 235 | | | | | 240 | |
| Phe | Ala | Met | Tyr | Arg | Pro | | | | | | | | | | |
| | | | | 245 | | | | | | | | | | | |

4210: 339
 4211: 849
 4212: DNA
 4213: Homo sapiens

4400: 339
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 caagacccta agaaccatca gccctcagct gcaactctc cctcccaagg 150
 atgacaaagg cctacacat ctatttggc agcagcttcc ttgcctaaa 200
 tcaggccagg ctatcagtc ctcttactt ggcacagga ctccagctga 250

agtactggg tadtattag attatatt tttttttt gctgtacct 330
 gctttttt aaatcaatt caatattat gatttaattt aaaatgcaga 350
 ttttaattt tadtatdgc ttttccatt caacacccac taatgatata 400
 acgattataa agttacttg caaaccttt acacgtaga ctgtcaagat 450
 ctgtgaate caaacctttt tdcaggtat cactacgcaa aaaggattat 500
 gtccgnaaa cyggggatga acaactgggt tgaatggagg ttgcactgtt 550
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 aggtgnggg tgcacgttag attctttca agactctgt cctcactcag 650
 ggattttca tttctttt ctactgtc caattcatgt tattttttt 700
 ccttccatt tacaactaaa actgacaga gccccagaaa taaatggttt 750
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 tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatc 849

<210> 340
 <211> 148
 <212> PRT
 <213> Homo sapiens

<100> 340
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 20 25 30
 Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
 35 40 45
 Asp Trp Leu Cys Leu Ala Phe Val Gln Ser Lys Phe Asn Ile Ser
 50 55 60
 Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
 65 70 75
 Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
 80 85 90
 Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
 95 100 105
 Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
 110 115 120
 Arg Gly Met Asn Asn Trp Val Gln Trp Arg Leu His Cys Ser Gly
 125 130 135
 Arg Trp Leu Ser Tyr Trp Leu Thr Gly Tyr Arg Leu Arg

401 341
 13
 DNA
 402 Artificial

4008
 401 Artificial Sequence
 402 1-13
 403 Synthetic construct.

409 341
 attcgaagg atgacaaagg cgc 23

4010 342
 4011 9
 4012 DNA
 4013 Artificial

4016
 4017 Artificial Sequence
 4018 1-9
 4019 Synthetic construct.

4027 341
 ggggaacagc ttctctgccc taaatcagg 29

4030 343
 4031 14
 4032 DNA
 4033 Artificial

4036
 4037 Artificial Sequence
 4038 1-14
 4039 Synthetic construct.

4040 343
 attcgaagg gcatcctgtc agcc 24

4046 344
 4047 14
 4048 DNA
 4049 Artificial

4050
 4051 Artificial Sequence
 4052 1-14
 4053 Synthetic construct.

4060 344
 attgcatgcat gcaagaaggt tggg 24

4066 345
 4067 45
 4068 DNA
 4069 Artificial

<120>
 <121> Artificial sequence
 <122> 1-45
 <123> Synthetic construct.

<400> 345
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<210> 346
 <211> 2575
 <212> cna
 <213> Homo sapiens

<400> 346
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 caaaggggga aagaaacacc tgaagaaat ggaatcatta tttttttccc 150
 aaggagaaaa cgggggtaaa gggagaaaag caattcaatt tgaagtcct 200
 gtgaatgggc ttccagaagg caattaaag aatcactca gagaggactt 250
 ggggtgaac ttgggtctgt tggttttct attataagta gaagcaggtc 300
 ttgcacacgc tgttggaaa tctcaggacc aggttaagta actggcagaa 350
 aaatttcag gtggaabaag caaccctat tctgtgtca gcttgaacaa 400
 ggcaggagcg ggagaaagct aacttgaca tcaactttt catttggcaa 450
 gttctagcaa catgtctcta aggaagcgat acaggcacag accatgcaga 500
 ctccagtttc tctgtctgt cctaatgtg ggaatggctc tgatgatggt 550
 ggcgatgttg caccctctcc accacacct gacacagact gtcacagccc 600
 aagccagcaa gcacagcct gaagccaggt accgcctgga ctttggggaa 650
 tccaggatt cgttactgga agctgaggat gagggtgaaq agtacagccc 700
 tctggagggc ctgcacccct ttatctcct gggggaggat cagctgtctg 750
 tggcgttggc cttaccocag gccagaagga accagagcca gggcaggaga 800
 ggtacaaact accgcctcat caagcagcca agcaggcagg ataaggaaac 850
 cccaaagagg gactggggg ctgatgagga cggggagggt tctgaagaag 900
 aggaattgac accgtttagc ctggacccac gtggcctcna ggagcactt 950
 agtgcoccca tccccctcna gagggtctg ccgaggtgc ggcacccact 1000
 ctctctcag agcaacctc agcaacctt accacagcc agctcactt 1050
 tctatttcca tctacaccc tctcactc tcttccaa tctacaccc 1100

atgtgagaa agtgcacaa atgttctgt aatggatca tttctatca 110
 ttaactttagc agacaaggac aatcagtc tgcctcaga atatatata 120
 caaggetaca ggggttgaac ttaacttaga qcaacaagag actgactgac 130
 atcagggecc ggtatgtagg ggcacacaga gccacogggg atatgtctat 140
 ctctatggat gccacttacc autgcaccc aggttggctg gagcactcc 150
 tcagcaaat agttggtgac aagacccagc tggatctctc ggtgatcaat 160
 gtgattgaat ggaagacttt caagtattac cctcaaaag acctgcagtg 170
 tgggtgtttg gactggaagc tggatttcca ctggaactt ttgcacagac 180
 atgtgaggaa ggccttcacg tccacataa gctccatcag caacactata 190
 ctgcacggac aggtggttgc catggacaga cattacttcc aaaaactac 200
 aggttatgar tctcttatgt cgtgcgagg tggtagaac ctgcaantgt 210
 attcaaggc ctggtctctt ggtggtcttg ttgaatcct tccctgctct 220
 gggtaggac acatctacca aaatcaggat tccattccc ccttcgacaa 230
 gtaggcacc ctgaggaaac gggthggat tgcagagac tggctggggt 240
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 aaggtgaga agcagactc catggacgc ttgcactgc aaaggagact 260
 gggttgtgg acattccact ggtttctggc taatgtctac cctgactgt 270
 accatctga accaggccc agttctctg gaaagctcca caaacctgga 280
 ctgggctct ctgcagactg ccaggcagaa gggacatcc tgggtgctcc 290
 catggtgttg gctccttgca gtgacagccg ccagcaacag taactgcagc 300
 acaccagcag gaaggagatt caatttggca gcacacagca cctgtacttt 310
 gctgtcaggc aggagcaggt gattcttcag aactgcacgg aggaaggcct 320
 ggcacccac cagcagcact gggacttcca ggagaatggg atgattgtcc 330
 acattctttc tggaaaatgc atggaagctg tggtcacaga aaacaataaa 340
 gatttgtacc tgcgtccgtg tcatggaaaa gcccgccagc actggcactt 350
 tgcacagata aatctgttgg atgaacata aatgtcaatc ttagaaggaa 360
 aagagaattt tggccatcaa aatccagctc caagtgaacg taagagactt 370
 atattttca tgaagctaat actttt ggt atgtgctctt tgggttaca 380
 atcaaaaat ctctatdaga caataaggga agtttctctt ttctacact 390

[illegible]

210: 34-

(111) 639

1993

(213) Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln
1 5 10 15

Phe Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val
 25 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
31 35 39

Phe Gly Glu Ser Glu Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
55 60 65

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
84 89 95

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
95 100 105

Arg Asn Gln Ser Glu Gly Arg Arg Gly Gly Ser Tyr Arg Leu Irg
 108 119 130

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
126 130 134

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Glu Leu Thr
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
156 175 189

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 295 310

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | His | Ser | Ile | Leu | Asp | Thr | Val | Pro | Arg | Ala | Phe | Leu | Lys | Glu |
| | | | | 215 | | | | | 220 | | | | | 225 |

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
240 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Iys Leu Leu
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

| | | |
|---|-------------------------|-----|
| Arg Ser Asn Lys Arg Leu Gly Ala Ile | Arg Ala Arg Met Leu Gly | 270 |
| Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His | | 280 |
| Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile | | 290 |
| Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile | | 300 |
| Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg | | 310 |
| Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro | | 320 |
| Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg | | 330 |
| Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr | | 340 |
| Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly | | 350 |
| Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly | | 360 |
| Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln | | 370 |
| Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg | | 380 |
| Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu | | 390 |
| Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala | | 400 |
| Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu | | 410 |
| Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu | | 420 |
| Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His | | 430 |
| Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp | | 440 |
| Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg | | 450 |
| Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys His Ile His Phe | | 460 |

| | | |
|---|-----|-----|
| 545 | 550 | 555 |
| Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val | | |
| 560 | 565 | 570 |
| Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln | | |
| 575 | 580 | 585 |
| His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser | | |
| 590 | 595 | 600 |
| Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu | | |
| 605 | 610 | 615 |
| Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe | | |
| 620 | 625 | 630 |
| Asp Gln Ile Asn Ala Val Asp Glu Arg | | |
| 635 | | |

<210> 548
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 548
 ggggaagtggtg tggccatgga cag 23

<210> 549
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 549
 ctgtcac*gc aaggagccaa cacc 24

<210> 550
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 550
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<210> 351
 <211> 2524
 <212> RNA
 <213> Homo sapiens

<400> 351
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 tcttcactct cccctcgagc ccacacagcc ccagcccgc ccctgtgtgc 200
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 ggcatctct gttcggggg cgtgggggag gttcgggccc ccagctctat 600
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 aagtctaccc ttccctccc ggaactccct ctgtccctcc ctttccctcc 2300
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 caggttcttc cctccctct actgggtttt ccaccttcc ccttcccttc 2400
 ttccctggct cctaggtgt gatataatt ttgtattat ctctttcttc 2450
 ctctgtggt gatcatctg aattactgt ggatgtaagt tcaaaaatt 2500
 tcaataaag cctttgcaag ataa 2524

<210> 452

<211> 243

<212> FRT

<213> Homo sapiens

<400> 452

Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly

1

5

10

15

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Leu | Leu | Leu | Leu | Gln | Leu | Pro | Ala | Pro | Ser | Ser | Ala | |
| | | | | 10 | | | | 35 | | | | | 30 | |
| Ser | Gln | Ile | Pro | Lys | Gly | Lys | Gln | Lys | Ala | Gln | Leu | Arg | Gln | Arg |
| | | | | 35 | | | | 40 | | | | | 45 | |
| Glu | Val | Val | Asp | Leu | Tyr | Asn | Gly | Met | Cys | Leu | Gln | Gly | Pro | Ala |
| | | | | 50 | | | | 55 | | | | | 60 | |
| Gly | Val | Pro | Gly | Arg | Asp | Gly | Ser | Pro | Gly | Ala | Asn | Val | Ile | Pro |
| | | | | 65 | | | | 70 | | | | | 75 | |
| Gly | Thr | Pro | Gly | Ile | Pro | Gly | Arg | Asp | Gly | Phe | Lys | Gly | Glu | Lys |
| | | | | 80 | | | | 85 | | | | | 90 | |
| Gly | Glu | Cys | Leu | Arg | Glu | Ser | Phe | Glu | Gln | Ser | Trp | Thr | Pro | Asn |
| | | | | 95 | | | | 100 | | | | | 105 | |
| Tyr | Lys | Gln | Cys | Ser | Trp | Ser | Ser | Leu | Asn | Tyr | Gly | Ile | Asp | Leu |
| | | | | 110 | | | | 115 | | | | | 120 | |
| Gly | Lys | Ile | Ala | Gln | Cys | Thr | Phe | Thr | Lys | Met | Arg | Ser | Asn | Ser |
| | | | | 125 | | | | 130 | | | | | 135 | |
| Ala | Leu | Arg | Val | Leu | Phe | Ser | Gly | Ser | Leu | Arg | Leu | Lys | Cys | Arg |
| | | | | 140 | | | | 145 | | | | | 150 | |
| Asn | Ala | Cys | Cys | Gln | Arg | Trp | Tyr | Phe | Thr | Phe | Asn | Gly | Ala | Gln |
| | | | | 155 | | | | 160 | | | | | 165 | |
| Cys | Ser | Gly | Pro | Leu | Pro | Ile | Glu | Ala | Ile | Ile | Tyr | Leu | Asp | Gln |
| | | | | 170 | | | | 175 | | | | | 180 | |
| Gly | Ser | Pro | Glu | Met | Asn | Ser | Thr | Ile | Asn | Ile | His | Arg | Thr | Ser |
| | | | | 185 | | | | 190 | | | | | 195 | |
| Ser | Val | Glu | Gly | Leu | Cys | Glu | Gly | Ile | Gly | Ala | Gly | Leu | Val | Asp |
| | | | | 200 | | | | 205 | | | | | 210 | |
| Val | Ala | Ile | Trp | Val | Gly | Thr | Cys | Ser | Asp | Tyr | Pro | Lys | Gly | Asp |
| | | | | 215 | | | | 220 | | | | | 225 | |
| Ala | Ser | Thr | Gly | Trp | Asn | Ser | Val | Ser | Arg | Ile | Ile | Ile | Glu | Glu |
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Leu Pro Lys

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<11> 480

<12> PNA

<13> Homo sapiens

<400> 353

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 ggaccagggc ggcggatccc tggggccggg cgtctatcgg gccatcgtga 350
 tggcggccct gctggccacc tggctggtgc tggcctcgt ggtcgtcgg 400
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 <111> 121
 <112> PRT
 <113> Homo sapiens

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 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
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100

101 Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
210 215

110 Ile Lys Leu Lys Glu Ser Glu Leu Pro Ala Leu Ala Ile Tyr
215 225

120 Thr Thr Leu Asp Asp Glu Trp Asp Thr Leu Ile Thr Ala Glu Val
230 235 240

130 Ser Val Glu His Val Glu Asn Phe Cys Asp Gly Phe Leu Ser Gly
245 250 255

140 Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
260 265 270

150 Glu Leu

210 359

211 24

212 DNA

213 Artificial

220

221 Artificial Sequence

222 1-24

223 Synthetic construct.

230 359

231 gagcagtc ccatactca tagc 24

240 360

241 20

242 DNA

243 Artificial

250

251 Artificial Sequence

252 1-20

253 Synthetic construct.

260 360

261 gagcagtc gataactgc 20

270 361

271 24

272 DNA

273 Artificial

280

281 Artificial Sequence

282 1-24

283 Synthetic construct.

290 361

291 gattataga atttctatc atgg 24

300 362

Artificial

3.3.1 Artificial Sequence

1-50

... synthetic construct.

 $\cdot 4 \cup \cup_2 = 462$ [illegible]

1. 363

1997

PLA

4. *Homo sapiens*

• 100 • 163

[illegible]

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cctcagggcg gaccggggt cagggaacgc gcgcgcgcgc 150

agtgqctgaa cgaatggaga gtcggccgaa tccggaggag tgatttcaga 200

ccacacacgc cagcgcctgc tctctctcgt actgagggag acgctttagc :50

letturaggio quadrato e quettoraggio talataggio aadagaadit 300

itotugocaa atogla:naa agugaadnta acutgaant te:anteta: 350

tagtaagact ggagggttga cctcagtctc ctggagcttc gaggcagagg 400

ggggcgaacac taatgtgtcg ttittccact actcccaagg gcaagtgtac 450

cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500

tgacaagaaa gatgcattcaa tcaacataga aaatatgagc ttctatacaga 550

atggacata tatctgtgat gtaaaagac ctcttgacat cgtttctca 600

cctggacaca ttaggtctta ttctgtagaa aaagagaatt tgcctgtgtt 650

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aaacacatt acactagctc cactacatc gagagttttt caccatttaa 600

[illegible]

100110799 atetacnac qneccagica tatatgaca attadaca 100

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

* 00

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Ile | Ser | Trp | Ala | Gly | Asp | Leu | Asp | Lys | Lys | Asp | Ala | Thr | Ile | |
| | | | | 110 | | | | | 115 | | | | | 120 | |
| Asp | Ile | Gln | Asn | Met | Gln | Phe | Ile | His | Asn | Gly | Thr | Tyr | Ile | Lys | |
| | | | | 125 | | | | | 130 | | | | | 135 | |
| Asp | Val | Lys | Asn | Pro | Pro | Asp | Ile | Val | Val | Gln | Pro | Gly | His | Ile | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Arg | Leu | Tyr | Val | Val | Glu | Lys | Glu | Asn | Leu | Pro | Val | Phe | Pro | Val | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Trp | Val | Val | Val | Gly | Ile | Val | Thr | Ala | Val | Val | Leu | Gly | Leu | Thr | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| Leu | Leu | Ile | Ser | Met | Ile | Leu | Ala | Val | Leu | Tyr | Arg | Arg | Lys | Asn | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Ser | Lys | Arg | Asp | Tyr | Thr | Gly | Cys | Ser | Thr | Ser | Glu | Ser | Leu | Ser | |
| | | | | 200 | | | | | 205 | | | | | 210 | |
| Pro | Val | Lys | Gln | Ala | Pro | Arg | Lys | Ser | Pro | Ser | Asp | Thr | Glu | Gly | |
| | | | | 215 | | | | | 220 | | | | | 225 | |
| Leu | Val | Lys | Ser | Leu | Pro | Ser | Gly | Ser | His | Gln | Gly | Pro | Val | Ile | |
| | | | | 230 | | | | | 235 | | | | | 240 | |
| Tyr | Ala | Gln | Leu | Asp | His | Ser | Gly | Gly | His | His | Ser | Asp | Lys | Ile | |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Asn | Lys | Ser | Glu | Ser | Val | Val | Tyr | Ala | Asp | Ile | Arg | Lys | Asn | | |
| | | | | 260 | | | | | 265 | | | | | | |

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 tggagctggg gctgggggtg ggctcggggg tgaagctggc aggtggggtg 200
 aggggcggg cccccggcca gtcccccgcg cccccggacc ctuaggcctc 250
 gctcttgccc gaggcggcac agggacagtc cctcgccccg tgatctccgc 300
 aaaccccgcc gccgacctgc ttcagttgct tggccagagg catccagacc 350
 atggtccccc tctgtccacg gatccagacc aggtggggcg caatggccat 400
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<010: 366
<011: 373
<012: PRT
<013: Homo sapiens

| | | | | | | | | | | | | | | |
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| Met | Tyr | Arg | Leu | Leu | Ser | Ala | Val | Thr | Ala | Arg | Ala | Ala | Ala | Pro |
| 1 | | | | 5 | | | | 10 | | | | | | 15 |
| Gly | Gly | Leu | Ala | Ser | Ser | Cys | Gly | Arg | Arg | Gly | Val | His | Gln | Arg |
| | | | | 20 | | | | 25 | | | | | | 30 |
| Ala | Gly | Leu | Pro | Pro | Leu | Gly | His | Gly | Trp | Val | Gly | Gly | Leu | Gly |
| | | | | 35 | | | | 40 | | | | | | 45 |
| Leu | Gly | Leu | Gly | Leu | Ala | Leu | Gly | Val | Lys | Leu | Ala | Gly | Gly | Leu |
| | | | | 50 | | | | 55 | | | | | | 60 |
| Arg | Gly | Ala | Ala | Pro | Ala | Gln | Ser | Pro | Ala | Ala | Pro | Asp | Pro | Gln |
| | | | | 65 | | | | 70 | | | | | | 75 |
| Ala | Ser | Pro | Leu | Ala | Gln | Pro | Pro | Ser | His | Gln | Ser | Leu | Ala | Pro |
| | | | | 80 | | | | 85 | | | | | | 90 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ser | Pro | Gln | Thr | Pro | Ala | Arg | Pro | Tyr | Ser | Arg | Cys | Phe | Ala | 105 |
| Arg | Ala | Ile | Glu | Ser | Ser | Arg | Asp | Leu | Leu | His | Arg | Ile | Lys | Asp | 110 |
| Glu | Val | Gly | Ala | Pro | Gly | Ile | Val | Val | Gly | Val | Ser | Val | Asp | Gly | 125 |
| Lys | Glu | Val | Trp | Ser | Glu | Gly | Leu | Gly | Tyr | Ala | Asp | Val | Glu | Asn | 140 |
| Arg | Val | Pro | Cys | Lys | Pro | Glu | Thr | Val | Met | Arg | Ile | Ala | Ser | Ile | 155 |
| Ser | Lys | Ser | Leu | Thr | Met | Val | Ala | Leu | Ala | Lys | Leu | Trp | Glu | Ala | 170 |
| Gly | Lys | Leu | Asp | Leu | Asp | Ile | Pro | Val | Gln | His | Tyr | Val | Pro | Glu | 185 |
| Phe | Pro | Glu | Lys | Gln | Tyr | Glu | Gly | Glu | Lys | Val | Ser | Val | Thr | Thr | 200 |
| Arg | Leu | Leu | Ile | Ser | His | Leu | Ser | Gly | Ile | Arg | His | Tyr | Glu | Lys | 215 |
| Asp | Ile | Lys | Lys | Val | Lys | Gln | Glu | Lys | Ala | Tyr | Lys | Ala | Leu | Lys | 230 |
| Met | Met | Lys | Glu | Asn | Val | Ala | Phe | Glu | Gln | Glu | Lys | Glu | Gly | Lys | 245 |
| Ser | Asn | Glu | Lys | Asn | Asp | Phe | Thr | Lys | Phe | Lys | Thr | Glu | Gln | Glu | 260 |
| Asn | Glu | Ala | Lys | Cys | Arg | Asn | Ser | Lys | Pro | Gly | Lys | Lys | Lys | Asn | 275 |
| Asp | Phe | Glu | Gln | Gly | Glu | Leu | Tyr | Leu | Arg | Glu | Lys | Phe | Glu | Asn | 290 |
| Ser | Ile | Glu | Ser | Leu | Arg | Leu | Phe | Lys | Asn | Asp | Pro | Leu | Phe | Phe | 305 |
| Lys | Pro | Gly | Ser | Gln | Phe | Leu | Tyr | Ser | Thr | Phe | Gly | Tyr | Thr | Leu | 320 |
| Leu | Ala | Ala | Ile | Val | Glu | Arg | Ala | Ser | Gly | Cys | Lys | Tyr | Leu | Arg | 335 |
| Tyr | Met | Gln | Lys | Ile | Phe | His | Asp | Leu | Asp | Met | Leu | Thr | Thr | Val | 350 |
| Gln | Glu | Glu | Asn | Gln | Pro | Val | Ile | Tyr | Asn | Arg | Ala | Arg | | | 365 |

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<111> 421
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<111> 369
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<111> 370
<111> 41
<111> DNA
<111> Artificial

<111> 422
<111> Artificial Sequence
<111> 1-41
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<111> 371
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<212> PRT

<213> Homo sapiens

<400> 372

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | Ser | Ala | Gly | Ala | Thr | Arg | Leu | Leu | Leu | Leu | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |
| Leu | Met | Ala | Val | Ala | Ala | Pro | Ser | Arg | Ala | Arg | Gly | Ser | Gly | Cys |
| | | | 20 | | | | | | 25 | | | | | 30 |
| Arg | Ala | Gly | Thr | Gly | Ala | Arg | Gly | Ala | Gly | Ala | Leu | Gly | Arg | Leu |
| | | | 35 | | | | | | 40 | | | | | 45 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Gln | Ala | Cys | Gly | Thr | Val | Gly | Leu | Leu | Leu | Glu | His | Ser | Phe | |
| | | | | 81 | | | | | 84 | | | | | 87 | |
| Gln | Ile | Asp | Asp | Ser | Ala | Asn | Phe | Arg | Lys | Arg | Gly | Ser | Leu | Leu | |
| | | | | 88 | | | | | 90 | | | | | 95 | |
| Trp | Asn | Gln | Gln | Asp | Gly | Thr | Leu | Ser | Leu | Ser | Gln | Arg | Gln | Leu | |
| | | | | 90 | | | | | 95 | | | | | 98 | |
| Ser | Glu | Glu | Glu | Arg | Gly | Arg | Leu | Arg | Asp | Val | Ala | Ala | Leu | Asn | |
| | | | | 99 | | | | | 100 | | | | | 105 | |
| Gly | Leu | Tyr | Arg | Val | Arg | Ile | Pro | Arg | Arg | Pro | Gly | Ala | Leu | Asp | |
| | | | | 110 | | | | | 115 | | | | | 120 | |
| Gly | Leu | Glu | Ala | Gly | Gly | Tyr | Val | Ser | Ser | Phe | Val | Pro | Ala | Cys | |
| | | | | 125 | | | | | 130 | | | | | 135 | |
| Ser | Leu | Val | Glu | Ser | His | Leu | Ser | Asp | Gln | Leu | Thr | Leu | His | Val | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Asp | Val | Ala | Gly | Asn | Val | Val | Gly | Val | Ser | Val | Val | Thr | His | Pro | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Gly | Gly | Cys | Arg | Gly | His | Glu | Val | Glu | Asp | Val | Asp | Leu | Glu | Leu | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| Phe | Asn | Thr | Ser | Val | Gln | Leu | Gln | Pro | Pro | Thr | Thr | Ala | Pro | Gly | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Pro | Glu | Thr | Ala | Ala | Phe | Ile | Glu | Arg | Leu | Glu | Met | Glu | Gln | Ala | |
| | | | | 200 | | | | | 205 | | | | | 210 | |
| Gln | Lys | Ala | Lys | Asn | Pro | Gln | Glu | Gln | Lys | Ser | Phe | Phe | Ala | Lys | |
| | | | | 215 | | | | | 220 | | | | | 225 | |
| Tyr | Trp | Met | Tyr | Ile | Ile | Pro | Val | Val | Leu | Phe | Leu | Met | Met | Ser | |
| | | | | 230 | | | | | 235 | | | | | 240 | |
| Gly | Ala | Pro | Asp | Thr | Gly | Gly | Gln | Gly | Gly | Gly | Gly | Gly | Gly | Gly | |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Gly | Gly | Gly | Gly | Ser | Gly | Leu | Cys | Cys | Val | Pro | Pro | Ser | Leu | | |
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 caccaggtgg tggggggg caccatgtg gtggtggt acgttacttt 150
 tctatgctgt ctggtggtt ggttgggtt agaa tcttca agatggggg 200

tggaaatgac tttagaata cctcctctct tgggtttta 240
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 tttttctac ctctataaac tttaaccaga ttactacttc ctggaagatc 350
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 caatgaattc cctgtgagt ggatccagc tacctttgat ggagctgctt 650
 tctggaaaca tgtgtgggt gtatgggag gtgtggcagc tgaggtgta 700
 cccagctgga tagggctggg goctgtagcg cctttgttg ctgcacatcc 750
 tctctgggt ctggagggg ccttggcctt tggaaactgg ggggagaaat 800
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 gggacagact ctggaattc agctatcgg gatgtacag atctctctgt 1550
 gctgaattt atgacttcc tctgtttct cctgcattg ctttctgttt 1600
 gctgaattt atgacttct atgactgca aagacttc ccaaatttc 1650

..... 1700

.....

.....

..... samples

.....

..... Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
5 10 15

..... Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
20 25 30

..... Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
35 40 45

..... Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
50 55 60

..... Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
65 70 75

..... Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
80 85 90

..... Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
95 100 105

..... Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
110 115 120

..... Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
125 130 135

..... Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
140 145 150

..... Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
155 160 165

..... Tyr Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
170 175 180

..... Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
185 190 195

..... Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
200 205 210

..... Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
215 220 225

..... Tyr Arg Arg Gln Arg Ala Ile Ser Arg Thr Cys Ala Gly Gly Leu
230 235 240

| | | | |
|---|-----|-----|-----|
| Val Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile | 245 | 250 | 255 |
| Ala Leu Ile Glu Ser Val Ile Phe Ile Phe Val Ile Leu Trp | 260 | 265 | 270 |
| Thr Arg Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe | 275 | 280 | 285 |
| Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg | 290 | 295 | 300 |
| Ala Thr Ser Lys Arg Tyr His Leu Glu Pro Met His Leu Leu | 305 | 310 | 315 |
| Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr | 320 | 325 | 330 |
| Ile Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile | 335 | 340 | 345 |
| Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser | 350 | 355 | 360 |
| Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala | 365 | 370 | 375 |
| Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys | 380 | 385 | 390 |
| Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr | 395 | 400 | 405 |
| Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu | 410 | 415 | 420 |
| Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu | 425 | 430 | 435 |
| Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu | 440 | 445 | 450 |

<210> 375

<211> 1098

<212> DNA

<213> Artificial

<400> 375

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gtcccccgg tgcctggcg ccacggctt ccgtatccat gattatttat 150

tttttttt tttttttt ttgggattt tttttttt caccgggaa 200

tttttttt tttttttt tttttttt ttgggattt ttgggattt 250

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Ala | Leu | Ileu | Tyr | Gly | Leu | Val | Val | Met | Ala | Gly | Val |
| | | | | | | | | | 10 | | | | | 15 |
| Ile | Pro | Ile | Gln | Gly | Gly | Ile | Leu | Asn | Leu | Asn | Lys | Met | Val | Lys |
| | | | | | | | | | 25 | | | | | 30 |
| Thr | Val | Thr | Gly | Lys | Met | Pro | Ile | Leu | Ser | Tyr | Trp | Pro | Tyr | Gly |
| | | | | 35 | | | | | 40 | | | | | 45 |
| Cys | His | Cys | Gly | Leu | Gly | Gly | Arg | Gly | Gln | Pro | Lys | Asp | Ala | Thr |
| | | | | 50 | | | | | 55 | | | | | 60 |
| Asn | Trp | Cys | Cys | Gln | Thr | His | Asp | Cys | Cys | Tyr | Asp | His | Leu | Lys |
| | | | | 65 | | | | | 70 | | | | | 75 |
| Thr | Gln | Gly | Cys | Gly | Ile | Tyr | Lys | Asp | Asn | Asn | Lys | Ser | Ser | Ile |
| | | | | 80 | | | | | 85 | | | | | 90 |
| His | Cys | Met | Asp | Leu | Ser | Gln | Arg | Tyr | Cys | Leu | Met | Ala | Val | Phe |
| | | | | 95 | | | | | 100 | | | | | 105 |
| Asn | Val | Ile | Tyr | Leu | Glu | Asn | Glu | Asp | Ser | Glu | | | | |
| | | | | 110 | | | | | 115 | | | | | |

<210> 379

<211> 24

<212> DNA

<213> Artificial

<214>

<215> Artificial Sequence

<216> 1-24

<217> Synthetic construct.

<218> 379

ttacctccac tgcctctgtgc tggg 24

<219> 380

<220> 24

<221> DNA

<222> Artificial

<223>

<224> Artificial Sequence

<225> 1-24

<226> Synthetic construct.

<227> 380

ccagagcagta tatcttcccc tggg 24

<228> 381

<229> 45

<230> DNA

<231> Artificial

<232>

<233> Artificial Sequence

<234> 1-45

1111> Synthetic construct.

1111> 764

atgacacaaatggtcaatgaatgaattggtgaatggaatgctc 45

1112> 383

1112> 764

1112> DNA

1112> Homo sapiens

1113> 762

atggttctctcctctctgcatgggggcccagggggcccagagagtataaa 50

tgatattctgaggggtccccgcacaaaccagagcccagtcacaggcgaga 100

cccttggaatgcacccggaaggagcccatgctctgtctgctcagctctg 150

ctcttgaggaaccccacctgggaggggaagatgtatggccctggaggagg 200

caactatttcagcaccactgagagctacgaacatgaatcacagggtctg 250

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gactctctggagctgaaactgggagccttggtgggaataccagggaagt 350

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gcattgctttgaatggaattatccactagaggagccgacactgagaca 600

ccagttatctccacatactcagcaaaactcaacgtgggtcgttaggggtg 650

gggtatggagccatcccaagctgagcccatctgtgtgggtggtggtgatggt 700

actggagtaaactgagtcgggacgtctgaatcgaatccaccataaataaaa 750

gcttctgcagaaaa 764

1110> 383

1111> 178

1112> FRT

1113> Homo sapiens

1400> 383

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Arg | Pro | Glu | Ala | Met | Leu | Leu | Leu | Leu | Thr | Leu | Ala | Leu |
| 1 | | | | | 5 | | | | 10 | | | | 15 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gly | Gly | Pro | Thr | Trp | Ala | Gly | Lys | Met | Tyr | Gly | Pro | Gly | Gly |
| | | 20 | | | | | | 25 | | | | | 30 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Lys | Tyr | Ile | Arg | Thr | Thr | Gln | Asp | Tyr | Asp | His | Glu | Ile | Thr |
| | | | 35 | | | | | 40 | | | | | 45 | |

101 Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
 102
 103 Leu Gly Asp Ser Thr Asp Val Lys Leu Gly Ala Leu Gly
 104
 105 Thr Gln Gln Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
 106
 107 Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
 108
 109 Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
 110
 111 Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
 112
 113 Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
 114
 115 Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
 116
 117 Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
 118

<210> 384
 <211> 2372
 <212> LNA
 <213> Homo sapiens

<400> 384
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 acctctgtgg ctgaactggg tgcctcatcag aggaactgct gggctatgga 100
 atacagatgt ggcagctcag gtgcgcccaa attgcctgga agaatacacc 150
 atcttttttcg ataagaagaa attgtacgat ccagtttttt ttttaacagg 200
 cccctcccca ccccccacaa aaactgtaaa gatgcacaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgcg gagaatgcgg 300
 tgttgggatt tatttggttt tgaagtgttc tgcgtggctg gcaaagaata 350
 atgttcacaa atcgttccat ctcccaaggc gtcccaatttt tottcttggg 400
 tctcagggag cctgactca ctacagtcca atgacaggg gctgtcatgc 450
 gactcttccc taagacaaag caaaagact agggacgacc ttggaacaat 500
 acgaatctt cgtttcaatg taattagact actgagcgga tcaactgtag 550
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aatataaa ttatagtaga tagattaaa tatattatit gattattat 150
 attatgatat tagattataa agattataa attataaa tatataatt 160
 attatataa accagattat attatataa attagattat accattatata 170
 attatattat gaaattgatt ttattagatt accagattat accagattat 180
 attatattat taatagattat tttattttt ttataattat attagattat 190
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 attatattat gattattat gattattat gattattat gattattat 500

...ggtatg agtataca aaaaacag atataaaa tggatgaa 215
 ...tataca agttatggt ccaaaatt ttttcccc ttatattat 220
 ...tattat agtatttc tttataga ttttcccc atggatatt 225
 ...ttataga ataatgga agttgaact ccgtttaat ataatacta 230
 ...ttataga ccattact attcattaa tggatatt gtttaagat 235
 ...aattttt tttatgtaa aaaaaaaa 237

100 385
 111 513
 213 PRT
 213 Homo sapiens

400 385
 Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
 1 5 10 15
 Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
 20 25 30
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
 35 40 45
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
 50 55 60
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
 65 70 75
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
 80 85 90
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
 95 100 105
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
 110 115 120
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
 125 130 135
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
 140 145 150
 Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
 155 160 165
 Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
 170 175 180
 Arg Asn Leu Gln Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
 185 190 195
 Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Gln Leu

| | | |
|---|-----|-----|
| 205 | 210 | 215 |
| Arg Leu Ala His Asn Ala Ile Ser Lys Leu Asn Leu Ala Leu Ile | 215 | 220 |
| Arg Leu Val Ser Leu Gln Asn Leu Tyr Leu Gln Trp Asn Lys | 235 | 240 |
| Ser Val Ile Gly Gln Thr Met Ser Trp Thr Trp Ser Ser Leu | 245 | 250 |
| Arg Leu Asp Leu Ser Gly Asn Glu Ile Glu Ala Ile Ser Gly | 260 | 265 |
| Pro Ser Val Ile Gln Cys Val Pro Asn Leu Gln Arg Leu Asn Leu | 275 | 280 |
| Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln Glu Ile Leu Asp Ser | 290 | 295 |
| Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala Gly Asn Ile Trp Glu | 305 | 310 |
| Cys Ser Arg Asn Ile Cys Ser Leu Val Asn Trp Leu Lys Ser Phe | 320 | 325 |
| Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys Ala Ser Pro Lys Glu | 335 | 340 |
| Leu Gln Gly Val Asn Val Ile Asp Ala Val Lys Asn Tyr Ser Ile | 350 | 355 |
| Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp Leu Ala Arg Ala Leu | 365 | 370 |
| Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro Arg Pro Lys His Glu | 380 | 385 |
| Ser Lys Pro Pro Leu Pro Pro Thr Val Gly Ala Thr Glu Pro Gly | 395 | 400 |
| Pro Glu Thr Asp Ala Asp Ala Glu His Ile Ser Phe His Lys Ile | 410 | 415 |
| Ile Ala Gly Ser Val Ala Leu Phe Leu Ser Val Leu Val Ile Leu | 425 | 430 |
| Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys | 440 | 445 |
| Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys | 455 | 460 |
| Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Gln Phe Tyr | 470 | 475 |
| Val Asp Tyr Lys Ser Thr Asn Thr Gln Thr Ser His Met Ser Leu | 485 | 490 |

Ser Gly Thr Gly Ile Lys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
 100 105 110

Lys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 386

ctcgggtctg aacagtttcg gggc 24

<210> 387

<211> 14

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-14

<223> Synthetic construct.

<400> 387

gtcccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 388

actcaattta catttacggt ctaactccct gagaaccatc cctgtacg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

aattcttgaga aagaagaaaa taaacacagg caccaaaaga ctatcttaag 50

tttaattgtccc tttaataatc tcaagatcca gacttttcaa tgcacctca 100

ggatctcaa ccatatggt ttggtttt cgtatatt ttgtgtgt 150

ctcttctctc ccatctcaaa caatcaat gttgttaaa ttatctca 200

aaatctta tggatggtat atcggatcc tcttcttct gtttcaggc 35
 aaatcttc tctgggttgc tgggtctc tggcttggc gctgattgag 360
 agtcccca atggtcttc aaggcctac cagggaatt cttggcttg 385
 agacttga ctctatttat aggaagaa cactatgag tccaaetgtt 400
 aaatttacc ttcaaatc aacccctgac ctatactc ttcctgctcc 410
 atgttttgc cctttaagct ccccaacctc atatgaadaa attgtaaaaa 500
 caactgatt ttagtggtg attatcaatt taaagtatt agacattctg 550
 taattccaaa acatcaatt taggaatgt tatttcagtt gttggaaatg 600
 tccagagatc tattcatata ctcttgaa ggaatttcc acaaaagaat 650
 gcatgttga aaaaattttg gctatggaa tgtttaata gtaaagtaac 700
 aggttttga tgtgtcactg ctgtatcata cttttatgct acacaaccac 750
 attaatgctt ctcactagt atccaaacag ccaacaatta ggtgcttgaa 800
 gtagtttcca tccatttag gactccactg cagtatacag cacaaccatt 850
 tctgctttaa actctttcct agcatgggtt ccataaaaaa tattataatt 900
 taacaatagc ccaagccgag aatccaaat gtctagaatc agaaccagaa 950
 agatagtatt tgaatgaagc tgaggggaaa cagtacgaaa aagaaaagt 1000
 tggagttgaa gggtaaaagg taaatgaaga gaaaagaaa aagattacaa 1050
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 cagcatcatg ctaagaacct tggcatagg tatctgttcc catgaggact 1300
 gcaaaagtag caatgagaca tcttcaagtg caattttggc agtggccatc 1350
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<210> 390
 <211> 146
 <212> PRT
 <213> Homo sapiens

<214> 390
 Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr
 1 10 15

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 100 | Leu | Cys | Leu | Pro | Leu | Phe | Gln | Leu | Val | Leu | Pro | Asp | |
| | 20 | | | | | | 30 | | | | | | |
| 110 | Cys | Glu | Glu | Asp | Glu | Met | Cys | Val | Asn | Tyr | Asn | Asp | Gln |
| | 35 | | | | | | 40 | | | | | | 45 |
| 120 | Asn | Gly | Trp | Tyr | Ile | Trp | Ile | Leu | Leu | Leu | Leu | Val | Leu |
| | 50 | | | | | | 55 | | | | | | 60 |
| 130 | Val | Ala | Ala | Leu | Leu | Cys | Gly | Ala | Val | Val | Leu | Cys | Leu |
| | 65 | | | | | | 70 | | | | | | 75 |
| 140 | Arg | Arg | Pro | Arg | Ile | Asp | Ser | His | Arg | Arg | Thr | Met | Ala |
| | 80 | | | | | | 85 | | | | | | 90 |
| 150 | Thr | Ala | Val | Gly | Asp | Leu | Asp | Ser | Ile | Tyr | Gly | Thr | Glu |
| | 95 | | | | | | 100 | | | | | | 105 |
| 160 | Ala | Val | Ser | Pro | Thr | Val | Gly | Ile | His | Leu | Gln | Thr | Gln |
| | 110 | | | | | | 115 | | | | | | 120 |
| 170 | Asp | Leu | Tyr | Pro | Val | Pro | Ala | Pro | Cys | Phe | Gly | Pro | Leu |
| | 125 | | | | | | 130 | | | | | | 135 |
| 180 | Pro | Pro | Pro | Tyr | Glu | Glu | Ile | Val | Lys | Thr | Thr | | |
| | 140 | | | | | | 145 | | | | | | |

1101 391

1111 26

1112 DNA

1113 Artificial

1121

1121 Artificial Sequence

1122 1-26

1123 Synthetic construct.

1400 391

1400 acatg taactcagg gatctc 26

1110 391

1111 23

1112 DNA

1113 Artificial

1120

1121 Artificial Sequence

1122 1-3

1123 Synthetic construct.

1400 391

1400 caaacatg gagcaggatc agg 23

1110 391

1111 19

1112 DNA

1113 Artificial

<220> Artificial Sequence
<221> 1-47
<223> Synthetic construct.

<400> 393
ccactgtgtc ctctgggacc taccatggc aaaaatgaa atgtatc 47

<210> 394
<211> 2349
<212> DNA
<213> Homo sapiens

<400> 394
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aagctcgtg ggggggggga cgtgagga aagcccaagg ccagctcagt 200
ctctctctac ttggggagag agagaagtc agatgccctt tttaaaactc 250
ctcttcaaaa ctcatctctt gggtagctga gttaatagag tggatacaac 300
cttgctgaag atgaagaata tacaatttg aggatattct ttctcttttt 350
tttcaagtc ttgatttgt gcttacctca agttacatt ttctagtcac 400
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tatgtctcag aaattgagtt tactgttgt tgtatttggc ctcatttggg 500
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 <113> Homo sapiens

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 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
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 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
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 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
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 35 40 45
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
 50 55 60
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
 65 70 75
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
 80 85 90
 Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
 95 100 105
 Arg Leu Arg Tyr Leu Gln Ser Leu Asp Leu Ser His Asn Gly Leu
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 Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
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Artificial

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Artificial Sequence

1-23

Synthetic construct.

<400> 349

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<410> 400

44

DNA

Artificial

<420>

Artificial Sequence

1-44

Synthetic construct.

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<410> 401

1571

DNA

Homo sapiens

<400> 401

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atgtcattct ctctctatc actgcaagt cctgctgttc caggcctac 200

ctctgggca ctaacgggg agccaggatg gggacagaat aaaggagcca 250

cgaactgtgc caccactcg cctcagaat ctgaactcag acctgaaatc 300

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tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

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ttctgagata cggggcagtg tgaagccaa agatggaaac attgacatca 550

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caatttctt tcttaattc cagaagcctc tctgtctc tctgacaa 750

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 <112> PRT
 <113> Homo sapiens

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 35 40 45
 Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
 50 55 60
 Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
 65 70 75
 Leu Ile Trp Ser Phe Asp Ile Arg Pro Tyr Met Lys Ala Ser Ser
 80 85 90

| | | | |
|---|-----|-----|-----|
| Asp Thr Trp Arg Ala Ser Tyr Ile Leu Leu Ser Gly Cys Ala Ala | 10 | 25 | 30 |
| Thr Thr Ala Glu Leu Ala Thr Ile Pro Leu Asp Leu Thr Lys Thr | 35 | 4 | 45 |
| Ala Ser Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp | 50 | 55 | 60 |
| Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala | 65 | 70 | 75 |
| Leu Tyr Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Lys | 80 | 85 | 90 |
| Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg | 95 | 100 | 105 |
| Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser | 110 | 115 | 120 |
| Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met | 125 | 130 | 135 |
| Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu | 140 | 145 | 150 |
| Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Lys | 155 | 160 | 165 |
| Lys Trp Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile | 170 | 175 | 180 |
| Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro | 185 | 190 | 195 |
| Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr | 200 | 205 | 210 |
| Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu | 215 | 220 | 225 |
| Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu | 230 | 235 | 240 |
| Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg | 245 | 250 | 255 |
| Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr | 260 | 265 | 270 |
| Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly | 275 | 280 | 285 |
| Ile Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met | 290 | 295 | 300 |
| Thr Trp Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg | | | |

100% Total

Initial Sequence-
... genetic construct.

1. *Attentus* *trisetatus* n. sp.

- 0.10: 45°C
- 0.15: 50°C
- 0.16: 100°C
- 0.130: Artificial

4220 .
4221 Artificial Sequence
422 1-34
4223 Synthetic construct.

400 - 408
magnetic transition frequency code 34

210 · 409
 <211 · 1487
 <212 · PNA
 <213 · Homo sapiens

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tagataattt tcatggaca gaatgtgaat gtattgaactg gagtgagaga 200
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Ile Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
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Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
 126 127 128 129 130 131 132 133 134 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
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Gly Arg Thr Glu Glu Leu Trp Thr
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2100 411
 2110 20
 2120 DNA
 2130 Artificial

2200
 2210 Artificial Sequence
 2220 1-20
 2230 Synthetic construct.

2300 411
 2310 *Streptococcus pyogenes* 20

2400 412
 2410 20
 2420 DNA
 2430 Artificial

2500
 2510 Artificial Sequence
 2520 1-20
 2530 Synthetic construct.

2600 412
 2610 *Streptococcus pyogenes* 20

2700 413
 2710 40
 2720 DNA
 2730 Artificial

2800
 2810 Artificial Sequence
 2820 1-40
 2830 Synthetic construct.

2900 413
 2910 *Streptococcus pyogenes* 20

3000 414

11.11.11
11.11.11
11.11.11 sapientia

414

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411-415
 411-414
 411-414
 411-414
 411-414

400-415

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Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
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Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
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Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
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Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105

Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120

Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135

Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150

Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165

Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180

Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195

Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210

Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
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4210-416
 4211-21
 4212-21
 4213-21
 4214-21

422-21
 422-21 Artificial Sequence

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 <100> 416
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 <100> 417
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 <110> Artificial

 <120>
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 <100> 418
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 <110> DNA
 <110> Artificial

 <120>
 <120> Artificial Sequence
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 <120> Synthetic construct.

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 <400> agctcag tgtggcctca tcaagc 26

 <100> 419
 <110> 24
 <110> DNA
 <110> Artificial

 <120>
 <120> Artificial Sequence
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 <120> Synthetic construct.

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 <400> tctgactct agtcacgca ggag 24

 <100> 420
 <110> 24
 <110> DNA
 <110> Artificial

 <120>
 <120> Artificial Sequence
 <120> 1-24
 <120> Synthetic construct.

 <400> 420
 <400> attcttca gacatctt ttc 24

... ..

Official Sequence
2.7 1-46
Synthetic construct.

46

| | |
|---|------------|
| 1 | 4.2 |
| 2 | 7.01 |
| 3 | 1.8A |
| 4 | m. sapiens |

- 2.1 unsure
- 2.2 100%
- 2.3 unknown base

400 - 422

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 <112> 387
 <113> Homo sapiens

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 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
 35 40 45
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
 50 55 60
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Gln
 65 70
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Leu Leu

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105 | |
| Ala Gln Leu His
110 | Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly
115 | 120 |
| Ser Glu His Gln
125 | Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His
130 | 135 |
| Ile Val His Tyr
140 | Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala
145 | 150 |
| Ala Glu Arg Pro
155 | Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu
160 | 165 |
| Val Gly Glu Thr
170 | Lys Asn Ile Ala Tyr Gln His Ile Leu Ser His
175 | 180 |
| Leu His Glu Val
185 | Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro
190 | 195 |
| Phe Asn Leu Arg
200 | Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe
205 | 210 |
| Arg Tyr Asn Gly
215 | Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val
220 | 225 |
| Leu Trp Thr Val
230 | Ile Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln
235 | 240 |
| Leu Glu Lys Leu
245 | Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Ile
250 | 255 |
| Ser Lys Leu Leu
260 | Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn
265 | 270 |
| Gln Arg Met Val
275 | Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr
280 | 285 |
| Thr Thr Gly Glu
290 | Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly
295 | 300 |
| Cys Leu Cys Leu
305 | Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile
310 | 315 |
| Arg Lys Lys Arg
320 | Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser
325 | 330 |
| Ala Gln Ala Thr
335 | Thr Glu Ala | |

*210- 424
 *211- 16
 *212- 1NA
 *213- Artificial

4240
4241 Artificial Sequence
4242 1-18
4243 Synthetic construct.

4400 424
gttaagtcgc tggccagc 18

4244 425
4245 18
4246 DNA
4247 Artificial

4248
4249 Artificial Sequence
4250 1-18
4251 Synthetic construct.

4400 425
ctgcatctgc ctgctgta 18

4248 426
4249 24
4250 DNA
4251 Artificial

4252
4253 Artificial Sequence
4254 1-24
4255 Synthetic construct.

4400 426
ctgcacgtga tggccattat tgtg 24

4256 427
4257 45
4258 DNA
4259 Artificial

4260
4261 Artificial Sequence
4262 1-45
4263 Synthetic construct.

4400 427
cagaaaccca tgatacccta ctgaacaccg aatccccctgg aagcc 45

4264 428
4265 1073
4266 DNA
4267 Homo sapiens

4400 428
aatttttcac cagagtaaaa ttggaagac aactgaaact tgactattgt 50
aatttttggc tcttgagaaa aaaggtatgc atctgaaa ca tcaagagtaa 100
aattttcattg ttctgtttt tggatcnaa tttttcatta ccaaatctca 150

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ile | Gly | Thr | Gln | Thr | His | Pro | Leu | Thr | Ile | Gly | Gly | Leu | Asn | 80 | 81 | 90 |
| Val | Gln | Gln | Gln | Leu | His | Pro | His | Val | Leu | Pro | Ile | Phe | Val | Thr | 95 | 100 | 105 |
| Gln | Leu | Gly | Ala | Gln | Gly | Thr | Ile | Leu | Ser | Ser | Gln | Glu | Leu | Pro | 110 | 115 | 120 |
| Gln | Ile | Phe | Thr | Ser | Leu | Ile | Ile | His | Ser | Leu | Phe | Pro | Gly | Gly | 125 | 130 | 135 |
| Ile | Leu | Pro | Thr | Ser | Gln | Ala | Gly | Ala | Asn | Pro | Asp | Val | Gln | Asp | 140 | 145 | 150 |
| Gly | Ser | Leu | Pro | Ala | Gly | Gly | Ala | Gly | Val | Asn | Pro | Ala | Thr | Gln | 155 | 160 | 165 |
| Gly | Thr | Pro | Ala | Gly | Arg | Leu | Pro | Thr | Pro | Ser | Gly | Thr | Asp | Asp | 170 | 175 | 180 |
| Asp | Phe | Ala | Val | Thr | Thr | Pro | Ala | Gly | Ile | Gln | Arg | Ser | Thr | His | 185 | 190 | 195 |
| Ala | Ile | Glu | Glu | Ala | Thr | Thr | Glu | Ser | Ala | Asn | Gly | Ile | Gln | | 200 | 205 | |

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 <311> 1257
 <312> DNA
 <313> Homo Sapien

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 cggagcgggg cggagccaga cggcgaccac gttcctctcc tgggtctcct 100
 ccgctccag ctcggcgctg ccgggcagcc gggagccatg cyaccccagg 150
 gccccgggcg ctcggcgag cggctccggg gctcctctgt gctcctgctg 200
 ctgcagctgc ccggcgcgtc gagcgccctc gagatccca aggggaagca 250
 aaaggcgag ctcgggcaga gggaggtggt ggacctgtat aatggaatgt 300
 gttacaagg gccagcagga gtgcctggtc gagacgggag cctcggggcc 350
 aatgttattc cgggtacacc tgggatccca gttcgggagc gattcaaaag 400
 agaaaagggg gaatgtctga gggaaaactt tgaggagtc ttgacacca 450
 actacaagca gtgttcctg acttcattga attatcgcat aatctctagg 500
 acaattcggg actgtacatt tacaaaatg cgttcaaaa gtgtctaaag 550
 gtttgttc actgtgca ttcctcaaa atggcaaat caatctctgc 600
 aacttcata ttcctctc atggaatg aatcttca atctctctgc 650

...taatttattt aaacaaagaa aacattttaa tgaattttaa 750
 ...atagatgattt ttctctgtgaa aggaattttaa gaaggattt 750
 ...agatgattt gctatctggg ttggaattt ttcaagattt 800
 ...atatttctac tggatggaat tcaatttctc gaacattt 850
 ...aaataaaa tgcatttatt ttcaatttctt aactattt 900
 ...ttggaatggt tcaattttaa gacattttaa ataagttt 950
 ...gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
 ...ctgttttttaa atctagcatt atttatttg cttaattcaa 1050
 ...aatattttt ttagttgggt agaatattt cttaattcaa 1100
 ...aatattt aaactataat ttggaatatt gttgtggtct ttgttttt 1150
 ...atagattt aggaattttaa aaaaaatata aaagctacca atctttgtac 1200
 ...aatgtgtaa tgttaagaat ttttttata tctgttaaatt aaaaattatt 1250
 tcaaca 1257

<P10> 431
 <P11> 243
 <P12> FRT
 <P13> Homo Sapien

<400> 431
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
 1 5 10 15
 Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20 25 30
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Gln Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Ile Thr Lys Met Arg Ser Asn Ser
 125 130 135

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Asp | Arg | Val | Leu | Ile | Ser | Gly | Ser | Leu | Arg | Leu | Lys | Cys | Arg | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Asn | Ala | Cys | Cys | Gln | Arg | Trp | Tyr | Phe | Thr | Phe | Asn | Gly | Ala | Glu | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Val | Ser | Gly | Pro | Leu | Pro | Ile | Glu | Ala | Ile | Ile | Tyr | Leu | Asp | Gln | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| Gly | Ser | Pro | Glu | Met | Asn | Ser | Thr | Ile | Asn | Ile | His | Arg | Thr | Ser | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Val | Val | Glu | Gly | Leu | Cys | Glu | Gly | Ile | Gly | Ala | Gly | Leu | Val | Asp | |
| | | | | 200 | | | | | 205 | | | | | 210 | |
| Val | Ala | Ile | Trp | Val | Gly | Thr | Cys | Ser | Asp | Tyr | Pro | Lys | Gly | Asp | |
| | | | | 215 | | | | | 220 | | | | | 225 | |
| Ala | Ser | Thr | Gly | Trp | Asn | Ser | Val | Ser | Arg | Ile | Ile | Ile | Glu | Glu | |
| | | | | 230 | | | | | 235 | | | | | 240 | |

Leu Pro Lys

210: 432
 211: 18
 211: DNA
 211: Artificial Sequence

220:
 220: Artificial Sequence

2400: 432
 2400: ctcagtgcc ctcaggaa 18

210: 433
 211: 21
 211: DNA
 211: Artificial Sequence

210:
 210: Synthetic oligonucleotide probe

2400: 433
 2400: cccaggacag ttatgaaaat a 21

210: 434
 211: 21
 211: DNA
 211: Artificial Sequence

210:
 210: Synthetic oligonucleotide probe

2400: 434
 2400: atgaggtat tctgaggtat a 21

210: 435

411 18
 411 DNA
 411 Artificial Sequence

 412
 412 Synthetic oligonucleotide probe

 440 435
 440 cctactgta ccaccatgt 19

 4210 436
 4211 21
 421 DNA
 421 Artificial Sequence

 422
 422 Synthetic oligonucleotide probe

 440 436
 440 actccaggca ccactctgttc tccc 24

 410 437
 411 19
 411 DNA
 411 Artificial Sequence

 423
 423 Synthetic oligonucleotide probe

 440 437
 440 gacacatggc attcaagtc 19

 410 438
 411 19
 411 DNA
 411 Artificial Sequence

 424
 424 Synthetic oligonucleotide probe

 440 438
 440 ctactggca aaggaagaa 19

 410 439
 411 21
 411 DNA
 411 Artificial Sequence

 425
 425 Synthetic oligonucleotide probe

 440 439
 440 cagcaccct ccagtccaag g 21

 410 440
 411 19
 411 DNA
 411 Artificial Sequence

6100 Synthetic oligonucleotide probe

6100 441

cttctgtgt ttctctaga 14

6101 441

611 20

611 DNA

611 Artificial Sequence

6102

6102 Synthetic oligonucleotide probe

6400 441

cttctctca gaggaccaat 20

6210 442

6211 25

6212 DNA

6213 Artificial Sequence

6220

6220 Synthetic oligonucleotide probe

6400 442

ctctccatca ctctccctag ctcca 25

6210 443

6211 24

6212 DNA

6213 Artificial Sequence

6220

6220 Synthetic oligonucleotide probe

6400 443

cttgcaggag ttaaagttcc aaga 24

6310 444

6311 18

6312 DNA

6313 Artificial Sequence

6320

6320 Synthetic oligonucleotide probe

6400 444

aaaggacacc gggatgtg 18

6310 445

6311 26

6312 DNA

6313 Artificial Sequence

6320

6320 Synthetic oligonucleotide probe

410 446
 catctctaga tgagatgata ga 26

 411 446
 411 20
 412 DNA
 413 Artificial Sequence

 420
 423 Synthetic oligonucleotide probe

 430 446
 catctctaga tgagatgata ga 22

 440 447
 441 20
 442 DNA
 443 Artificial Sequence

 450
 453 Synthetic oligonucleotide probe

 460 447
 caggactgag cgattgttta 20

 470 448
 471 21
 472 DNA
 473 Artificial Sequence

 480
 483 Synthetic oligonucleotide probe

 490 448
 caaaggccca agtaccggac c 21

 500 449
 501 18
 502 DNA
 503 Artificial Sequence

 510
 513 Synthetic oligonucleotide probe

 520 449
 ccagacctca gccaggaa 18

 530 450
 531 18
 532 DNA
 533 Artificial Sequence

 540
 543 Synthetic oligonucleotide probe

 550 450
 cactctctga cactctga 18

<10> 451
<11> 27
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<200>
<210> Synthetic oligonucleotide probe

<400> 451
atgacaagc atttttttga atc 23

<10> 452
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<400> 452
ctctccccc ccttttttct ttgttt 26

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ctctgtgcc cacagtga 18

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ccatgectgc tcagccaaga a 21

<10> 455
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<13> Artificial Sequence

<200>
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<400> 455
caggaattat ccaacattac att 23

<10> 456
<11> 23
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the Lincolnshire tide gauge

JACCCATTI LC

Official Sequence

• Synthetic dinucleotide probe

11/11/2014, 10:00:00 AM

- 1: The
- 2: 3
- 3: NA
- 4: Artificial Sequence

2.2.3. Synthetic oligonucleotide probe

100 - 158
 100 - 158

| | |
|------|---------------------|
| 1010 | 459 |
| 1011 | 72 |
| 1012 | DNA |
| 1013 | Artificial Sequence |

123 Synthetic oligonucleotide probe

100 459
meagaggt ggaactatc ta 22

| | |
|------|---------------------|
| 1.10 | 460 |
| 1.11 | 23 |
| 1.12 | RNA |
| 1.13 | Artificial Sequence |

14. Synthetic oligonucleotides probe

^a 400, 460,
1000 nm; 1000 nm; and 29

210 - 161
211 - 16
212 - 18A
213 - 18B
214 - 18C
215 - 18D
216 - 18E
217 - 18F
218 - 18G
219 - 18H
220 - 18I
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222 - 18K
223 - 18L
224 - 18M
225 - 18N
226 - 18O
227 - 18P
228 - 18Q
229 - 18R
230 - 18S
231 - 18T
232 - 18U
233 - 18V
234 - 18W
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236 - 18Y
237 - 18Z
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618 - 33Q
619 -

1

6100 Synthetic oligonucleotide probe

611 461

cttttctgttgcagggaa 18

612 462

611 18

612 DNA

613 Artificial Sequence

620

622 Synthetic oligonucleotide probe

610 462

tcattgtctcctcccatc 19

610 463

611 27

612 DNA

613 Artificial Sequence

621

623 Synthetic oligonucleotide probe

610 463

ctctattttat tttctgtgtct ccccatc 27

610 464

611 18

612 DNA

613 Artificial Sequence

620

623 Synthetic oligonucleotide probe

610 464

cggacatctct tggagtac 13

610 465

611 20

612 DNA

613 Artificial Sequence

620

623 Synthetic oligonucleotide probe

610 465

ctcccatctac cagcaggagta 20

610 466

611 23

612 DNA

613 Artificial Sequence

620

623 Synthetic oligonucleotide probe

610 466

4000: 471
4000: DNA
4000: Artificial Sequence

4000: Synthetic oligonucleotide probe

4000: 472
4000: Artificial Sequence 24

4000: 473
4000: 19
4000: DNA
4000: Artificial Sequence

4000: Synthetic oligonucleotide probe

4000: 474
4000: agggcaagg tgagtcac 19

4000: 474
4000: 20
4000: DNA
4000: Artificial Sequence

4000: Synthetic oligonucleotide probe

4000: 474
4000: ccttctgagg agccctatgc 20

4000: 475
4000: 22
4000: DNA
4000: Artificial Sequence

4000: Synthetic oligonucleotide probe

4000: 475
4000: tccaggtaga cccacttca gg 22

4000: 476
4000: 24
4000: DNA
4000: Artificial Sequence

4000: Synthetic oligonucleotide probe

4000: 476
4000: gggaggttta taggcccacat ctgg 24

4000: 477
4000: 10
4000: DNA
4000: Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

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